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Submitted (16-AUG-1997) Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@dmb.med.keio.ac.jp, Tel:03-3351-2370, Fax:03-3351-2370)
Location/Qualifiers
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Shimizu, N.
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APCRDGGELICCDGCPRAFHLACLSPPLREIBSGTWRCGSCLQATVTQFVQPDSAAFLEDTGLRCR
DEPVETPLPPGLRSAGEEVRGPPGGFDVLRCTHCAAFHWRCHFPAGTSRPGTGLRCR
RCSGDVTPAPVEGVLAPSPARLAPGPAKDDTASHEPALHRDDLESLLSEHTFDGILQW
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/gene="APECED"
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REFERENCE AUTHORS CQ731863 Sequence 177 CQ731863 CQ731863.1 Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo. Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. 1545 bp DNA 17797 from Patent WO02068579. GI:42309567 PAT 03-FEB-2004

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                                                                                                AGCCACCCGTGGAGACCCCGCTCCCCCCGGGGCTTAGGTCGGCGGGAGAGGAGGTAAGAG
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CTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCCTGCACCCCCTACTGT
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TITLE
JOURNAL REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 3 AB006685 DEFINITION FOCUS TITLE 2 (bases 1 to 1463)
Shimizu,N.
Direct Eubmission
Direct Submission
Submitted (16-AUG-1997) Nobuyoshi Shimizu, Keio University
of Medicine, Department of Molecular Biology; 35 Shinanomac
Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@dmb.med.keio. Nagamine, K., Peterson, P., Scott, H.S., Kudoh, J., Minoshima, S., Heino, M., Krohn, K.J.E., Lalioti, M.D., Mullis, P.E., Antonarakis, S.E., Kawasaki, K., Asakawa, S., Ito, F. and Shimizu Positional cloning of the APECED gene Positional Cloning of the APECED gene Nat. Genet. 17 (4), 393-398 (1997) Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Nat. Genet. 98061086 Homo sapiens APECED mRNA 9398839 APECED; AIRE-3 AB006685.1 GI:2696622 AB006685 (sites) 1463 A for AIRE-3, mRNA linear , complete cds. Hominidae; Euteleostomi; Homo. PRI Shimizu, 13-DEC-1997

Shinanomachi,

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/map="21q22.3"
/sex="male"
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(mol type="mRNA"
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stage="3-yr-old"
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Pred. No. 3.3e-189;
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1 (bases 1 to 2245)
Yaspo, M. and Lehrach, H.
Yaspo, M. and Lehrach, H.
NUCLEIC ACID MOLECULE ENCODING A (POLY) PEPTIDE CO-SEGREGATING
MUTLATED FORM WITH AUTOINMUNE POLYENDOCRINOPATHY CANDIDIASIS
ECTODERMAL DYSTROPHY (APECED)
Patent: WO 9918197-A 1 15-APR-1999;
                                                                                                    unclassified.
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                                          GCCGGCCGGCTGGGATCAAGAAGGGGACAGCGCCACCTCTTGTCAGTGCTCGGCTGTAAA
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Lehrach,H. and Yaspo,M.L.
Lehrach,H. and Yaspo,M.L.
An autoimmune disease, APBCED, caused by mutations
featuring two PHD-type zinc finger domains
Nat. Genet. 17, 399-403 (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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VYKHLEAPPSAAFLPGLDSSALHPLLCVGPEGQQNLAPGARCGVCGDGTDVLRCTHCA
AAFHNRCHFPAGTSRFGTLRCRSCGGDVTPAFVEGVLAPSPARLAPGPAKDDTASHE
PALHRDDLESLLSEHTFDGILQWAIQSMARPAAPPPS" Score 1023.6; DB 9; Length Pred. No. 3.2e-189; O; Mismatches 4; Indels 0; Gaps 1650 1055 1170 1050 1475 1890 1415 1830 1355 1770 1295 1710 1235 1175 1590 1115 1530 1470 1410 1350 1290 1230 1110 995 935 875 815 695 635 575 755

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                                                                                                                    Direct Submission Submitted (16-AUG-1997) Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (B-mail:shimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370(ex.2720), Fax:81-3-3351-2370)
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Shimizu, N.
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Nat. Genet. 17 (4), 393-398 (1997)
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AIRE-1, AIRE-2,
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                                                                                                                                                                                                                                                                     JOIN(8965. .9148,9455. .9910,11002. .11101,11693. .11725, 11808. .11875,12489. .12610,13100. .13202,15082. .15144, 16355. .16688)
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4707. 16426

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/note="alternative splicing"
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                                                                                             TTGGTGTACAGTTCCGGGGCCCCTGGAACGCAGCCTGCAAGAAACCGGGTTTTCTTC
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QEPPVETPLPPGLRSAGEEPRCQGWTPRPCTPYCVWVLRVSRTWLLVRVAGCAEMVRT
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Direct Submission
Submitted (17-JUL-1998) Steffen Hennig, MPING, Abt. Lehrach, Max
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Lee, Y.S., Francis, F.,
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Nat. Genet. 17, 399-403 (1997)
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complement (2208.
/note="(GAAAA)n"
complement (2235.
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                                                    /note="Alusq/x"
                                                                                      complement (1824.
/note="AluSg"
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/note="Aluy"
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Location/Qualifiers
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/note="GC_rich"	/notes MIR"	_region c	<b>~ μ</b> ·	repeat_region 17663 .17959 /note="Aluy"	repeat_region complement(1737917530)	repeat_region complement(1709017375)	<pre>/note="AluSg/x" repeat_region complement(1693317084) /note="MIT1A1"</pre>	repeat_region 1672616931	region compleme	repeat_region complement(1539815700) /note="Alusg"	repeat_region complement(1501915394)	repeat_region complement(1472215018)	repeat_region complement (1436014720)	repeat_region complement(1406114357)	repeat_region complement (1375114060)	repeat_region 1358513738	repeat_region 1328913582 /note="AluSx"	<pre>repeat_region complement(1288713178) /note="AluSc"</pre>	repeat_region 12193. 12880 /note="11"	repeat_region complements (1199312079)	repeat_region complement(1150111878)	repeat_region complement(1091811215)  /notes "Alusx"	repeat_region 1000000000000000000000000000000000000	repeat_region 1020610439	/note="(GAAAA)n" repeat_region complement(77998101)		repeat_region 7445. 7729	repeat_region complement (71077409)	repeat_region complement(6805, .7106)	repeat_region 65316761	7 · ·	repeat_region complements (57225820)	repeat_region complement(53325634)	/note="AluSx" repeat_region complement(31093382) /note="AluY"
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complement (3479335417)	1400000 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3429134854 /gene="AIRE" /number=14	/gene="AIRE" /number=13	/number=12 /number=12 3302233084	31040 . 31142 /gene "AIRE"	complement (3087230983)	3042830549 /gene="AIRE" /number=11	/gene="AIRE" /number=10	T'A	/number=8 /number=8 2894329042	/ 10mbet=/ 27736 27851 / 10mbet=/ 127851	/gene="AIRE" /gene="AIRE"	85	2629826443 2629826443	complement (2595626114)  /note="MLT1A1"	complement (2579525875)	/gene="AIRE" /number=5	/number=4 2498625099	710m307-7-7 24158 24232 /gene "AIRE"	1 2 .	/number=2 /number=2 /361923774	2319823372 /gene_"AIRE"	YIRHIRKE SAKK LEGUUSSALITELUK WEEGGAMAKKUS WILGUKKASKSUS I PAPVEGVLAPSPARLAPGPAKDDTASHEPALHRDDLESLLSEHTEDGILQWAIQSMAR DAADERG	GSVERFUHLESDEVLHÖVINEUBLAVLKUSSELI LLUGLEVAR HIJACUSETUKELESDE ERGESCONT WRCSSCLQATVQEVQPRAEEPREPGEPVETEL PEGLESGAGEEVRGPPGEPLAGMDTTL WROSSCLQATVQEVQPRAEEPREPGEPVETENGAGETUKENSAGETUKENTATUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSAGETUKENSA	KPPKKPESSAEQQRLPLGNGJQTMSASVQRAVAMSSGDVPGARGAVEGILLIQQVPESG GSKKCIQVGGEPYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQ GSKKCIQVGGEPYTPSKFEDSGSGKNKARSSSGPKPLVRAKGAQGAAPGGGEARLGQQ	DVDLSQPRKGRKPPAVPKALVPPPRLPTKRKASEBARAAPAALTPRGTASPGSQLKA	/translation="MATDAALRRLLRLHRTBIAVAVDSAFPLLHALADHDVVPBDKFQ	/db_wref="GOA:043918"	/ COUCHE PERIOR   PER	/gene="AIRE"	28943. 29042,29633. 29815,30428. 30459,31040. 31142, 33022. 33084.34291. 34362)	70mm225-* join(2264822779,2319823372,2361923774,2415824232, 24986	, p.	2252934854 /gene="AIRE" 2252922779

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                                                                                                       Submitted (12-JAN-2000) Nobuyoshi Shimizu, Keio University, So
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku,
160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 42133)
Shimizu,N., Kudoh,J. and Shibuya,K.
Homo sapiens genomic DNA, chromosome 21, clone D4G11, MX1-D21S171
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Shimizu,N., Kudoh,J. and Shibuya,K.
Direct Submission
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Direct Submission
Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717429.
The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan,
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* e.mail: nshimizu@dmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
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* URL: http://hgp.gsc.riken.go.jp/
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    Institute of Molecular Biotechnology, Genome Analysis,

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The Chimpanzee Chromosome 22 Sequencing Consortium cons
*Chinese National Human Genome Center at Shanghai,
Shanghai, China;
*GBF, Dept. of Genome Analysis, Braunschweig, Germany;
*Institute of Molecular Biotechnology, Jena, Germany;
*KRIBB Genome Research Center, Daejeon, Korea;
*MAX-Planck-Institute for Molecular Genetics, Berlin,
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center,
                                                                                                                                                                                                                                      2 (bases 1 to 143192)
Kube,M., Sudbrak,R., Mueller,I.,
Heitmann,K., Gimmel,V., Beck,A.,
Yaspo,M.L. and Reinhardt,R.
                                                                                                                                                                                                                                                                                                                                                                 The Chimpanzee Chromosome 22 Sequencing Consortium DNA sequence of chimpanzee chromosome 22 and its e
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 143192)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 462.4; DB 9;
Pred. No. 2.7e-80;
0; Mismatches 11;
                                                                                                                                                                                                                                                              Thiel, J., Klages, S., Borzym, K., Ben Kahla, A., Lehrach, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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           Taipei
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                                                                                        Query Match
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                                              183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.chori.org/bacpac/chimpanzee251.htm. The clone may be obtained from Pieter J. de Jong and coworkers (http://www.chori.org/bacpac). VECTOR: pTARBAC2.1
IMPORTANT: This sequence is not the entire insert of clone CH251-479II3 It may be shorter because we sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The CHORI-251 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa, K. et al.Genomics 52:1-8). The DNA from the chimpanzee ('Clint') was obtained from the Yerkes Primate Center in Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu, Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assembly was confirmed by restriction digest. ----
Neighboring sequence information:
This clone is overlapped by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characteristics are described at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *RIKEN Genomic Sciences Center, Yokohama, Japan.
AGGTCGGGAGAGACCTCCCTGGGCCTGGCCCACTGCCCCTGTGAGGAAGGGTTCGTGTGG, 37969
                                         AGGTCGGGAGAGACCTCCCTGGGCCTGGCCCCACTGCCCTGTGAGGAAGGGTTCATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: DUCLB; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990229 Consensus quality: 143190 bases at least Q40 Consensus quality: 143192 bases at least Q30 Consensus quality: 143192 bases at least Q30 Consensus quality: 143192 bases at least Q30 Quality coverage: 25.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: CH251-479I13
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                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1. .14090
                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-061A04"
                                                                                                                                                                                                                                                                                   organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                             note="overlapping clone"
141389. .>143192
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Pred. No. 4.7e-78;
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                                                                                                                                                                                                                                                                               3 (bases 1 to 1656)
Ruan,Q.G., Wang C.Y., Shi,J.D. and She,J.X.
Direct Submission
Submitted (17-FEB-1999) Pathology, Universi
                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1656)
Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G., Huang,Y.Q.,
Detter,J.C., Davoodi-Sermiromi,A. and She,J.X.
Complete genomic sequence, gene structure and localizati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detter, J.C. and She, J.X. Chromosomal localization and complete genomic sequence of the murine autoimmune regulator gene (Aire) Autoimmunity 31 (1), 47-53 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                mouse Aire gene
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Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                       /gene="Aire"
                                                                /map="between D10Mit31 and
l. .>1656
                                                                                                                                                                      organism="Mus musculus"
|mol_type="mRNA"
                                                                                                                               db_xref="taxon:10090"
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                                                                                                            chromosome="10"
                                                                                                                                                        strain="SJL"
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mRNA, partial ROD 26-OCT-2001

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GCTGGCCCCAGCCCCGCCCCGCCTGGCCCTGGGCCTGCCAA-----GGATGACACTGC
                                                                                                                                         TCTCCGCTGCAAATCCTGCTGCAGACTCGACTCCCACGCCAGGCACACCGGGCGAAGC
                                                                                                                                                                                                                                   CGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGG
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TKPPKKPDRILBSQHLPLGNIGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQOVFES
GRSKKCIQVGGEPYTPMKREDPSGILKNIKARSGSSLKPVVRAKGAQVITJERGRBGXVG
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AVTVNILLAPHPAAPLLEPSALCPLLSAKNGRBPGPAPSARCSVCGDGTPEVLRCARCS
AAFHWRCHFPTAAARPGTNLRCKSCSADSTPIPGTPGBAVPTSGPRPAPGLAKVGDDS
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/protein_id="AAF36481.1"
/db_xref="GI:7108573"
/translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
QETLRLKEKEGCPQAFHALLSWLLTRDSGAILDFWRILFKDYNLERYSRLHSILDGFP
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Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G., Huang,Y.Q.,
Detter,J.C., Davoodi-Sermiromi,A. and She,J.X.
Complete genomic sequence, gene structure and localizati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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/product = "autoimmune regulator"
/protein id="AAF36482.1"
/protein id="AAF36482.1"
/db xref="GI:7108575"
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/translation="WAGGGOMLRRILLFUNFWILFKDYNLERYSRLHSILDGFP
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GRSKKCIQVGGEFYTPNKFBDPSGNLKNKARSGSSLKFVVRAKGAQVTIPGRDEQKVG
QQCGVPPLFSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
GLWRCSCCLQGRVQQNLSQPEVSRPELPAET9ILVGLRSASEKTRGPSRELKASSDA
AVTYVNLLAPHPAAPLLEFSALCFLLSAGNEGRPFAPSARCSVCBGTEVLRCCHCA
AAFHRGCHFTAAARRGTNLRCKSCSADSTFTEGTPGEAVFTSGPRAPGLAKVGDDS
ASHDPVLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                             codon_start=1
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|strain="NOD"
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Patent: WO 9918197-A 10 15-APR-1999;
MAX PLANCK GESELLSCHAFT (DE); YASPO MARIE LAURE (DE)
1. 1659
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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0; Mismatches 244
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Mus musculus mRNA for Aire I
AJ132243
AJ132243.1 GI:4456674
Aire gene; Aire protein.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                      580;
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Submitted (14-JAN-1999) Karin B., Max Planck Institute for
Molecular Genetics, Ihnestrasse 73, Berlin D-14195, German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blechschmidt,K., Schweiger,M., Wertz,K., Poulson,R., Christensen,H.M., Rosenthal,A., Lehrach,H. and Yaspo. The mouse Aire gene: comparative genomic sequencing, organization, and expression Genome Res. 9 (2), 158-166 (1999) 99148139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular Genetics, Ihnestrasse
Location/Qualifiers
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Mammalia; Eutheria; Rodentia;
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                      CTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCCTGTCCCCTCCGGCA
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/codon_start=1
/codon_start=1
/product="Aire protein"
/protein_id="CAB36909.1"
/protein_id="CAB36909.1"
/protein_id="CAB36909.1"
/db_xref="GI:4456675"
/db_xref="GOA:Q920E3"
/db_xref="GO
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ASHDPVLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"
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/chromosome="10"
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Pred. No. 5.8e-65;
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                                                                                                                                                    Halonen,M., Pelto-Huikko,M.,
Ulmanen,I. and Kolmer,M.
Expression of the mouse AIRE
                                                                                              Kolmer, M.
                                                                                                                                  Unpublished
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CT 1648
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                                                                                                              (bases 1 to 1906)
Location/Qualifiers
                                                                                                                                                                                          Palvimo,J.,
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Direct Submission
Submitted (14-JUL-1999) Kolmer M., Department of Human Molec
Genetics, National Public Health Institute, Mannerheimintie
Helsinki, FIN-00300, FINLAND
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Sciurognathi; Muridae;
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/product="APECED protein"
/protein id="CAB66141.1"
/db_xref="GI:6706793"
/db_xref="GOA:09Z0E3"
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KOVDLAQSRKGRKPLAGPKAAVLPPRPPTKRKALEEPRATPPATLASKSYSSPOSHLK
TKPPKKPDGNLESQHLPLGNGIQTMAASVQRATVTVASGDVPGTRGAVEGILIQQVPES
GRSKKCIQVGGEFYTPNKFEDPSGILKNKARSGSSLKFVVRAKGAQVTI PGRDEQKVG
QQGVPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
GLWRCSCCLQGRVQQNLSQPEVSR PELPAETFILVGLRSASEKTRGFSRELKASSDA
AVTYNILLAFHPAAFLLEFSALCPLLSAGNEGREPAPSARCSVCGDGTEVLRCHCA
AAFHWRCHFPTAAARPGTNLRCKSCSADSTPTGTPGEAVFTSGFRPAFGLAKVGDDS
ASHDPVLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"
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/mol_type="mRNA"
/db_xref="taxon:10090"
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/db_xref="Swiss-Prot:Q9Z0E3"
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Ruan, O.G., Wang, C.Y., Shi, J.D. and She, J.X.
Expression and alternative splicing of the regulator gene (Aire)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-FEB-1999) Pathology, University Archer Road, Gainesville, FL 32610, USA
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Ruan, O.G., Wang, C.Y.,
Direct Submission
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Mammalia; Eutheria; Rodentia;
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58. .1704
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/note="alternatively spliced pro
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/mol_type="mRNA"
/strain="B6"
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                        Mua
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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(Aire)
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Wang,C.Y., Shi,J.D., Davoodi-Semiromi,A.
Direct Submission
Submitted (21-JUL-1998) Pathology, Immuno
Medicine, University of Florida, 1600 SW
FL 32610, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manualsa, Territory (bases 1 to 1936)

1 (bases 1 to 1936)

Wang, C.Y., Shi, J.D., Davoodi-Semiromi, A. and She, J.X.

Cloning of Aire, the mouse homologue of the autoimmune regulator Cloning of Aire, the mouse homologue polyglandular syndrome tyrops) Gene responsible for autoimmune polyglandular syndrome tyrops.
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                                                                                                                                                                                                                                                                                                                                                    CCAGGTTAACCAGAAGAACGAGGATGAGTGTGCCGTGTGCCACGACGAGGTGAGCTCAT
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                                                           ACTGAGGTCAGCTTCAGAGAAAAACCAGGGGCCCATCCAGGGAGCTCAAAAGCCAGCTCTGA
                                                                                        GCTTAGGTCGGCGGGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGA 811
                                                                                                                                  GTCCCAGCCTGAGGTGTCCAGGCCCCCGGAGCTACCTGCAGAGACCCCCGATCCTCGTGGG
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GETLELKEKEGCPQAFHALLSWILTROSGAILDFWRILFKONTLERYSELHSILDGHF
KDVDLMQSRKGRKENLAGPKAAVLPFRPPFKREALEERPAFTPARTLASKSVSBOSHLK
TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVFES
GRSKKCIQVGGEFYTPKKFEDPSGNLKNKARSGSSLKFVVRAKGAQVFIDFGDEQKVG
QQCGYPPLPSLPSEQPQNQKNEDECAVCHDGGELICCDGCPRAFFHLACLSPPHQEIPS
GLWRCSCCLQGRVQQNLSQPEVSRPPELPAETPILVGLRSASEKTRGPSRELKASSDA
AVTYVNLLAPHPAPLLEPSALCPLLSAGNUSGPBAPSARCSVCGDGTEVLRCAHCA
AAFHNCHFFTTAAARPGTNLRCKSCSADSTFTPGTPGBAPSARCSVGDGTEVLRCAHCA
AAFHNCHFFTTAAARPGTNLRCKSCSGADSTFTPGTPGBAPGTAFGPBAPGLAKVGDDDS
ASHDPVLHRDDLESLLNEHSFDGILQMAIQSMSRPLAETPPFSS"
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58. .1716
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/product="autoimmune regulator"
/protein_id="AAD20444.1"
/db_xref="GI:4426599"
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/strain="B6"
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68.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 385.6; DB 10;
Pred. No. 5.7e-65;
0; Mismatches 244;
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1600 SW Archer Road, Gainesville,
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; I Mammalla; Eucheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 1921)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse auto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF128117

Mus musculus autoimmune regulator spliced product 1d, complete cds.

AF128117
                                                                                                                                                                                                                                                                                       Submitted (12-FEB-1999) Pathology, University Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                                                                                                                                                                               regulator gene (Aire)
Unpublished
                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                               Ruan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                       Q.G., Wang, C.Y., Shi, J.D. and
/function="transcription factor"
/note="alternatively spliced pro
/codon starte1
/product="autoimmune regulator"
                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                            map="between D10Mit31 and
                                                                                                                                                                 /db_xref="taxon:10090"
/chromosome="10"
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                                                                         'gene="Aire"
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(Aire) mRNA, alternatively
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/db_xref="GI:7108536"

/db_xref="GI:7108536"

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GRSKKCIQVGGEFYTPNKFEDDPSGNLKNKARSGSSLKPVVRAKGAGCRDEXVEGQCG

VPPLPSLPSEPQVNQNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPSGLWRC

SCCLQGRVQQNLSQPEVSRPPELPAETFILVGLRSASEKTRGPSRELKASSDAAVTTV

NLLAPHPAAPLLESSALCPLLSAGNEGRPGPAPSATCSVCGDGTEVLRCAHCAAFHW

RCHFPTAAARFGTNLRCKSCSADSTPTPGTPGEAVPTSGPRPAPGLAKVGDDSASHDP

VLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"
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Pred. No. 5e-63;
0; Mismatches 2
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Ruan,O.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse autoimmune regulator gene (Aire)
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Archer Road, Gainesville, FL 32610,
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AF128115
AF128115.1 GI:7108531
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Mus musculus
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Ruan,Q.G., Wang,C.Y., Shi,J.D. and
Direct Submission
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                                             GAGAGGAGGTAAGAGGTCCACCTGGGGAAACCCCTAGCCGGCATGGACACGACTCTTGTCT
                                                                                        TGTCCAGGCCCCCGGAGCTACCTGCAGAGACCCCGATCCTCGTGGGACTGAGGTCAGCTT
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/product="autoimmune regulator"
/db_xref="d1:7108532"
/db_xref="d1:7108532"
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/pr
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/mol_type="mRNA"
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note="alternatively spliced pro
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Pred. No. 5e-63;
0; Mismatches 204;
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X80853
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Biochem. Mol. Biol. Int.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Common promoter features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphofructokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levanon,D., Brandeis,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1549935
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to
  /rpt_family="Alu"
1251. .1597
                                                                                                                                                                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                    /clone_lib="chromosome 21 enriched
(Cytometry 7;411-417;1986)"
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                           product="phosphofructokinase"
                                               note="1/2Aluv"
                                                                                        note="liver type"
                                                                                                                                                                                                 map="21q22.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                              2586)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTACATAGGGACGACCTGGAGTCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGGCGCTGCCACTTCCCGACGGCCGCCGCCCGGCCGGGGACCAATCTCCGCTGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCACCGGGACGGGCCTGCGCTGCAGAT
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phosphofructokinase.
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genomic library
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TITLE
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AF128121
LOCUS
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KEYWORDS
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Best Local Similarity
Matches 336; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1744)
Ruan,O.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF128121
1744 bp
Mus musculus autoimmune regulator
spliced product 2d, complete cds.
                                                                                                                                                                                                                                                                      Submitted (12-FEB-1999) Pathology, University of Florida, 1600 Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1744)
Ruan, Q.G., Wang, C.Y., Shi, J.D. and
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF128121.1 GI:7108543
                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                 regulator gene (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF128121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Alu"
2471. .2526
/function="transcription factor"
/note="alternatively spliced pro
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58. .1524
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                                                                                                                                               /map="between D10Mit31 and D10Mit10"
                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                              strain="B6"
                                                                                   gene="Aire"
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 336; DB 9;
Pred. No. 2.5e-55;
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(Aire) mRNA, alternatively
                                                                                                                                                                                                                                                                                                                     She, J.X.
                                                    product
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                                                     2d 7
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닭 S 밁 S 片 5 밁 S 밁 S 밁 Ś 片

Snoo

FEATURES

source

/mol\_type="mRNA"
/strain="B6"
/db\_xref="taxon:10090" organism="Mus musculus" location/Qualifiers

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JOURNAL
REFERENCE
AUTHORS
TITLE
                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 25
AF128120
                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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Best Local Similarity
Matches 269; Conserv
                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   969 GACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTTCCCAGCC
                                     2 (bases 1 to 1747)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and
Direct Submission
                                                                                                                                                                                                                                                                                                                       AF128120
Mus musculus autoimmune regulator spliced product 2c, complete cds.
AF128120
Submitted (12-FEB-1999) Pathology, University Archer Road, Gainesville, FL 32610, USA
                                                                                                Unpublished
                                                                                                                                        Ruan, Q.G., Wang, C.Y., Shi, J.D. and She, J.X. Expression and alternative splicing of the
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 1747)
                                                                                                                                                                                                                                          Mus musculus
                                                                                                                         regulator gene (Aire)
                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                       AF128120.1
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llarity 69.9%;
Conservative
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TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVFBS
GRSKKCIQVGGBEYTPNKFEDPSGNLKNKARSGSSLKPVVRAKQAGRDEQKVGQQCG
GRSKKCIQVGGBEYTPNKFEDPSGNLKNKARSGSSLKPVVRAKQAGRDEQKVGQQCG
VPPLPSLPSEPQVNQNBSDEAVCHDGGBLICTOGCPBAFHLACLSPPLGEISGLMCC
SCCLQGRVQQNLSQPBVSRPPELPAETFGPAFSARCSVCGDGTEVLRCAHCAAAFHWR
CHFPTAAARPGTNLRCKSCSADSTFYPGTFGEAVFTSGPRAPGLAKVGDDSASHDPV
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Pred. No. 7.1e
0; Mismatches
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; Murinae; Mus
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RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                            AF128119 1756 bp
Mus musculus autoimmune regulator
spliced product 2b, complete cds.
                                                         1 (bases 1 to 1756)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the
regulator gene (Aire)
Unpublished
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                   AF128119.1 GI:7108539
                                                                                                                                                                                                                                                                                                                                                                                   spliced product
AF128119
                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCATCCAGAGCATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCCTTCTGAGCGAGCACCTTCGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCC 1256
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GETLRLKEKEGCPQAFHALLSWLLTRDSGAILDFWRILFKDYMLERYSRLHSILDGFP
KDVDLNQSRKGRKPLAGPKAAVLPFRPTKKALLEEPRATPPATLASKSYSSPGSHLK
TKPFKKEDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVFGTRGAVEGILIQQVFES
GRSKKCIQVGGEFYTFNKFEDFSGNLKNKARSGSSLKFVVRAKGAQGRDEQKVGQQCG
VPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCFRAFHLACLSFPLQEIFSGLWR
CSCCLQGRVQQNLSQFEVSRFPELPAETFFPAFSARCSVCGDGTEVLRCAHCAAAFHW
RCHFFTAAARFGTNLRCKSCSADSTFTFGTFGEBAVFTSGFRPAFGLAKVGDDSASHDP
VLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"
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/function="transcription fact
/note="alternatively spliced
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/product="autoimmune regulator"
/protein_id="AAP36465.1"
/db_xref="GI:7108542"
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Pred. No. 7.1e-24;
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(Aire) mRNA, alternatively
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                                                                                                                                                                                                             Euteleostomi;
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RESULT 27 AF128118

27

ACCESSION DEFINITION Locus

AP128118 1759 bp
Mus musculus autoimmune regulator
spliced product 2a, complete cds.
AF128118

mRNA (Aire)

mRNA, alternatively linear

ROD 29-FEB-2000

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity
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Ruan, Q.G., Wang, C.Y., Shi, J.D. and in Direct Submission
Submitted (12-FEB-1999) Pathology, 1
Archer Road, Gainesville, FL 32610,
                                                                                                                                                                                                                                                                                                                     GCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTG------
                                                                                                                                                                                                                                                                                                                                                                                       GACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCAGCC
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CGCCCGCTGGCCGAGACACCACCCT 1525
                                  CGTCCGGCGGCCCCCTCCT 1281
                                                                         TCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCATCCAGAGCATGTCA
                                                                                                                                            GCCAAGGTAGGGACGACTCTGCTAGTCACGACCCTGTTCTACATAGGGACGACCTGGAG
                                                                                                                                                                                   GCCAA-----GGATGACACTGCCAGTCACGAGCCCCGCTCTGCACAGGGATGACCTGGAG
                                                                                                                                                                                                                       ACGCCAGGCACACCGGGCGAAGCTGTACCCACCTCTGGGCCCCGTCCAGCACCTGGGCTT
                                                                                                                                                                                                                                                      GCCGCCGCCCGGGGACCAATCTCCGCTGCAAATCCTGCTCTGCAGACTCGACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="autoimmune regulator"
/product="autoimmune regulator"
/product="alf36464.1"
/protein_id="AAF36464.1"
/db_xref="Gl;7108540"
/translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF
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TKPPKKPDGNLESQHLPLGGNIQTMAASVQRAVTVASGDVPGTRGAVEGILIQQVFES
GRSKKCIQVGGEFYTPNKFEDPSGNLKNKASGSSLEVCHDGAPHLACLSPFLQEIFKQ
QQCGVPPLFSLDSEQVQNLSQPEVSRPPELPAETPGBPSARCSVCGDGTEVLACLSPFLQAIFK
QQCGVPPLPSLDSEQVQNLSQPEVSRPPELPAETPGFPSARCSVCGDGTEVLACLSPFLQAIF
FHWRCIFFFTAAARFGTWLRCKSCSADSTFTFOTFGBAVFTSGFRPAFGLAKVGDDSAS
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58. .1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDPVLHRDDLESLLNEHSFDGILQWAIQSMSRPLAETPPFSS"
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/mol_type="mRNA"
/strain="B6"
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/note="alternatively spl;
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Submitted (12-FEB-1999) Pathology, University of Florida, 1600
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Ruan, O.G., Wang, C.Y., Shi, J.D. and She, J.X.
Expression and alternative splicing of the mouse autoimmune
regulator gene (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1759)
Ruan, Q.G., Wang, C.Y.,
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                      GACGTGCTGCGGTGTACTCACTGCGCCGCCTGCCTTCCACTGGCGCTGCCACTTCCCAGCC 1028
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                                                                                                  GCCAA-----GGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAG
                                                                                                                                                                                                                                                                                                                 GAGGTGTTGCGGTGTGCACACTGTGCCGCTTGCCACTGGCGCTGCCACTTCCCGACG
                                    TCCCTTCTGAGCGAGCACACCTTCGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCC
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                                                                                                                                                                                                                                                                      GGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTG-----
TCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCATCCAGAGCATGTCA
                                                                         GCCAAGGTAGGGGACGACTCTGCTAGTCACGACCCTGTTCTACATAGGGACGACCTGGAG
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/product="autoimmune regulator"
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QCGVPFLPSLPSEPQNNQKNBDECAVCHDGGELICCDGCRAFHLACLSFPLGEIFS
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/function="transcription factor"
/note="alternatively spliced pro
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/mol_type="mRNA"
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Location/Qualifiers
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Pred. No. 7.1e-24;
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Ruan,Q.G., Wang,C.Y.,
Direct Submission
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Unpublished
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GATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCA 691
                                                                                                                                 CTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCCTGTCCCCCTCCGGGA 631
                                                                                                                                                                                                                                                             TTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCAT 571
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/db_xref="GI=7108550"
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/strain="B6"
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/note="alternatively spliced pro
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1. .1625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 159;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shi,J.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
.8e-21;
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                                                                                                                                               Query Match
Best Local Similarity
Matches 213; Conserv
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                                  512 TTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCAT 571
                                                                                                           452 TGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTGCATGGGCGTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1637)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF128122 1637 bp
Mus musculus autoimmune regulator
spliced product 3a, complete cds.
AF128122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-FEB-1999) Pathology, | Archer Road, Gainesville, FL 32610,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF128122.1 GI:7108545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCCGGGCAGAGGAGCCCCCGGCCCCAGGAGCCACCCGTGGAGACCCCCGCTCCCCCCGGG 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCCCCAGTGGCCTCTGGAGATGCTCCTGCCTGCCTCCAGGGCAGAGTCCAACAGAACCT 1097
CCAGGTTAACCAGAAGAACGAGGATGAGTGTGCCGTGTGCCACGACGGAGGTGAGCTCAT
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nn,Q.G., Wang,C.Y., Shi,J.D. and
                                                                                                                                                 Conservative
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KDVDLNQSRKGRKPLAGPKAAVLPPRPPTKRKALEEPRATPPATLAVSKILTIQOVGSHLK
TKPPKKPDGNLESQHLPLGNGIQTMAASVQRAVTVASGDVPGTRQAEGILIQOVGS
GRSKKCIQVGGEFYTPNKFEDPSGNLKNKARSGSSLKPVVRAKGAQVTIPGRDEQKVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Aire"
58. .1287
                                                                                                                                                                                                                                                          QQCGVPPLPSLPSEPQVNQKNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPS
GLWRCSCCLQGRVQQNLSQPEVSRPPELPAETPDQSPLQILLCRLDSHARHTGRSCTH
                                                                                                                                                                                                                                         LWAPSSTWACQGRGRLC"
                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="autoimmune regulator"
/protein_id="AAP36467.1"
/db_xref="GI:7108546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="transcription factor"
/note="alternatively spliced pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         map="between D10Mit31 and D10Mit10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                        translation="MAGGDGMLRRLLRLHRTEIAVAIDSAFPLLHALADHDVVPEDKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="B6"
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                                                                                                                                               Score 159; DB 10;
Pred. No. 7.8e-21;
0; Mismatches 90;
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(Aire)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              product
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526 AGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCT

Matches 179;

Conservative

0,

Mismatches

50;

<u>,</u>

Gaps

0

585

Query Match Best Local Similarity

9.6%;

Score 149; DB 10; Pred. No. 6.9e-19;

Length 1622; Indels

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AF128125
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Ruan,Q.G., Wang,C.Y., Shi,J.D.
Direct Submission
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Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse
regulator gene (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF128125 1622 bp
Mus musculus autoimmune regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-FEB-1999) Pathology, University of Florida, 1600 SW
Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCT 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCT 754
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Location/Qualifiers
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                                                                                                                       /codon_start=1
/product="autoimmune regulator"
/prodein_id="Autoimmune regulator"
/protein_id="Autoimmune regulator"
/pro
                                   STWACQGRGRLC"
                                                               SCCLQGRVQQNLSQPEVSRPPELPAETPDQSPLQILLCRLDSHARHTGRSCTHLWAPS
                                                                                              VPPLPSLPSEPQVNQNEDECAVCHDGGELICCDGCPRAFHLACLSPPLQEIPSGLWRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="B6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="between
                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="alternatively spliced product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="transcription factor"
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                                                                      Query Match
Best Local S
Matches 179
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               941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1834)
Ruan,Q.G., Wang,C.Y., Shi,J.D. and She,J.X.
Expression and alternative splicing of the mouse autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-FEB-1999) Pathology, University of Archer Road, Gainesville, FL 32610, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1634)
Ruan, Q.G., Wang, C.Y., Shi, J.D. and
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spliced product 3b, complete cds.
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Mus musculus autoimmune regulator
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                     Similarity
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               AGAACGAGGATGAGTGTGCCGTGTGCCACGACGAGGTGAGCTCATCTGTTGTGACGGCT
                               TCTGGAGATGCTCCTGCTCCAGGGCAGAGTCCAACAGAACCTGTCCCAGCCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCCCGGGCCTTCCACCTGGCTTGCCTGTCCCCACCTCTGCAGGAGATCCCCAGTGGCC 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus (house mouse)
                                                                                                                                          / tränslation="maggdgmlrrllrlhrteiavaidsaffilhaladhdvipedkf

/ tränslation="maggdgmlrrllrlhrteiavaidsaffilherysrlhsidgfp

KDVDLNQSrkgurplagpraavlpprpptyrkaleefrattpaytlasksysspeghty

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GRSKKCIQVGGEFYTPNKFEDFSGNLKNKARSGSSLKFVVRAKGAQVTIPGRDEQXVG

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LMRCSCCLQGRVQQNLSQPEVSRPPELPAETPDQSPLQIILCRLDSHARHTGRSCTHL

WAPPSSTWACQGRGRLC"
                                                                                                                                                                                                                                                                                                                                                               /gene="Aire"
58. .1284
                                                                                                                                                                                                                                                        /codon_start=1
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/db_xref="GI:7108548"
                                                                                                                                                                                                                                                                                                                  function="transcription factor"
/note="alternatively spliced pro
                                                                                                                                                                                                                                                                                                                                                 /gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                        map="between D10Mit31 and D10Mit10"
                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _type="mRNA"
                                                                                    9.6%;
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                                                                     Score 149; DB 10;
Pred. No. 6.9e-19;
0; Mismatches 50;
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(Aire)
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Query Match
Best Local Similarity
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Sequence
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                             Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with Patent: WO 0200928-A 66 03-JAN-2002;
                                                                                                                             synthetic construct synthetic construct
                                                                                                                                                                                                      Sequence 66 from Patent AX344995
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               Epigenomics AG (DE)
                                                                                                                                                                                       AX344995.1
                                                                                                            artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   artificial sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
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/db_xref="taxon:32630"
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location/Qualifiers
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Pred. No. 4.7e-13;
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BV089377
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             Query Match
Best Local S
Matches 119
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1 (bases 1 to 581)
1 (bases, Liao, G., Cheng, J., Nguyen, A., Bach, C., Puech, A., McPherson, J.D., Foernzler, D. and Peltz, G.
Mus musculus SNPs
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                                                                                                                                                                                                                                                                   Primer A: No primer submitted.
                                                                                                                                                                                                                                                                                                                                                                           Contact: Jonathan Usuka
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus
                                                                                                                                                                                                                                                                                                   Email: Jonathan.Usuka@roche.com
                                                                                                                                                                                                                                                                                                                              3431 Hillview Ave, Mailstop S3-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                            Palo Alto
                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/msp="1.0-11206-10631-CAAA01111727.1.1.11206"
/clone_lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15
different strains-of mice (as of October 1, 2003). Those
strains include AJJ, A/HeJ, -129/Sv, AXR/J, B10.D2-H2/OSNJ,
BALB/CByJ, BALB/CJ, C3H/HeJ, C57BL/6J,-CAST/Ei, DBA/2J,
MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon.32630"
                                                                                                                                                                                                                                                      Location/Qualifiers
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             Score 96.6; DB 11
Pred. No. 1.3e-08;
0; Mismatches 19
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Pred. No. 8e-10;
0; Mismatches
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                               Palo Alto, CA 94024, USA
                                      DB 11;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; 1 (Dases 1 to 18351)
Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.G., Huang,Y. Detter,J.C. and She,J.X.
Chromosomal localization and complete genomic sequence murine autoimmune regulator gene (Aire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-NOV-1998) Department of Pathology, Laboratory Medicine, University of Florida, 1600 Room D6-15, Gainesville, FL 32610, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 18351)
Shi,J.D., Wang,C.Y., Marron,M.P., Ruan,Q.Q.,
Detter,J.C. and She,J.X.
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Autoimmunity 31 (1), 47-53 (1999)
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/product="autoimmune regulator"
join(4918. .5052,5365. .5539,5769. .5925,6219. .6292,
join(4918. .8052,5365. .5539,5769. .10488,
6740. .6853,8274. .8422,8611. .8691,10373. .10488,
11577. .11676,12530. .12706,13659. .13780,13879. .13987,
16489. .16557,18058. .18138)
                                                                                                                                                                                                                                                                                                                                                                                                        join(<4918. .5052,5365. .539,5769. .5925,6219. .6292,
6740. .6853,8274. .8422,8611. .8651,10373. .10488,
11577. .11676,12530. .12706,13659. .13780,13879. .13987,
16489. .16557,18058. .>18138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <4918. .>18138
/gene="Aire"
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                                                                                                                                                                                                                                                                                                                                                                                      /gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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ORGANISM
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VERSION
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MEDLINE
PUBMED
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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                                                                                                                                                                                                                                                                                                 repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10351 TGGGTCCCTCTTGCCTG-GTCAGAAGAACGAGGATGAGTGCCGTGTGCCACGACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502 TGGGCGTCTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGGCCGTGTGTCGGGACGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ007715
AJ007715.1 GI:3550507
AJ007715.1 GI:3550507
Alre gene; autoimmune regulator.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-AUG-1998) Division of Medical Genetics, University Geneva, 1, Rue Michel-Servet, Geneva, GE 1211, Switzerland Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mittaz, L., Rossier, C., Heino, M., Peterson, P., Krohn, K.J., Morris, M.A., Kudoh, J., Shimizu, N., Antonarakis, S.E. and S. Isolation and characterization of the mouse Aire gene Blochem. Blophys. Res. Commun. 255 (2), 483-490 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMU007715
Mus musculus Aire gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mittaz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTGCAGGAGATCCCCAG 10488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCTCCGGGAGATCCCCAG 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAGCTCATCTGTTGTGACGGCTGTCCCCGGGCCTTCCACCTGGCTTGCCTGTCCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 18616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
/gene="Aire"
/gene="Aire"
/rpt_family="SINE/84"
/rpt_family="SINE/84"
/oin(2970. .3416.3417. .3591,3592. .3820,3821. .3976,
/oin(2970. .3416.3417. .3591,3592. .3820,3821. .3976,
/oin(2970. .3416.3417. .3591,3494. .6413,
/oin(2970. .3581. .4432,4433. .4879,4880. .4993,4994. .6413,
/oin(2970. .3581. .4432,4433. .4879,4880. .4993,4994. .6413,
/oin(2970. .3591. .66131.6832. .3595,8750. .3621,
/oin(2970. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621. .3621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(1347. .2537,5851. .6020,6085. .6232,6233, .6296,7758. .7893,10146. .10356,10359. .10551, .10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10541,10
                                                                                                                                                                                                                                                                                                                                                                                                                /rpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comp]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (2281. .2291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Aire"
complement(1347. .1546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="Aire"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="129ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xref="taxon:10090"
                                                                                                                                                                                                                                                                                                     family="SINE/Alu"
Tement (2425. .2537)
                                                                                                                                                                                                                                                                                                                                                                                                                family="SINE/B4"
Tement(2292. .2424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="DNA/MER1_type"
lement(1912. .2128)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="SINE/B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96.6; DB 10;
Pred. No. 7.4e-09;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROD 11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scott, H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                    intron
                                                                                                                                                                                                                                                                                                                                                                                                                repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                        repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intron
                                                           6563. .6750
/gene="Aire"
                                                                                                                                                                                                        /rpt_family="SINE/B2"
complement(6085. .6232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (5851. .6020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4433. .4879
/gene="Aire"
                                                                                                                                                                                                                                                                                                     complement (6233. .6296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <2970. .3104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4880. .4993
/gene="Aire"
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9710. .9809
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Best Local Similarity 85.6%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                    TITLE
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Blechschmidt, K., Schweiger, M., Wertz, K., Poulson, R., Christensen, H.M., Rosenthal, A., Lehrach, H. and Yaspo, M.L. The mouse Aire gene: comparative genomic sequencing, gene organization, and expression genome Res. 9 (2), 158-166 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46872)
1 (bases 1, Bjoersee, P., Perheentupa, J., Horelli-Kuitunen, N., Palconen, J., Bjoersee, P., Lee, Y.S., Francis, F., Hennig, S., Thiel, C., Lehrach, H. and Yaspo, M.L.
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46872 bp DNA linear ROD 05-AUG-19: Mus musculus cosmid MPMGc121L12287 containing the syntenic region of the human AIRE gene, complete sequence.
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Blechschmidt, K., Huong-My, C., Nordsiek, G., Drescher, B., Rosenthal, A. and Yaspo, M.-L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-JUN-1998) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGCGTCTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCG
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172 bp frame: 2 phase: 1"
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library number 121 (RZPD-berlin). Cloning vector Lawrist
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	ı	repeat_region	1 1 1	repeat_region	repeat_region	exon	exon	exult		exon	exon	gene	misc_feature	repeat_region	exon	exon	repeat_region	repeat_region	misc_feature	exon	
/gene="mouse nomotogue of the numen Africa gene (Alka) Acc. No. 297990)" /number=6 /evidence=experimental	erimental	/evidence=not_experimental /rpt_family="ĀluSg" complement(1282012881)	1 (0	/evidence=not experimental /rpt_family="MLTID" complement(1253912600)	/number=3 /evidence=experimental complement(1224112306)	/evidence=experimental 1146511578 /gene="Mouse homologue of the human APECED gene (AIRE; Acc. No. 297990)"	/evidence=experimental 10943. 11017 /gene="Mouse homologue of the human APBCED gene (AIRE; Acc. No. 297990)" /number=4	/genne="Mouse homologue of the human APECED gene (AIRE; Acc. No. 297990)" /number=3	o. Z97990)" r=2 nce=experimental	/ Humber - 1 / evidence=experimental / evidence=experimental 1000210176 / gene="Mouse homologue of the human APECED gene (AIRE;	95559689 /gene="Mouse homologue of the human APECED gene (AIRE; Acc. No. Z97990)"	<pre>/evidence=not_experimental 9555, .22828 /gene="Mouse homologue of the human APECED gene (AIRE; Acc. No. Z97990)"</pre>	/rpc ramily="Alusg" 93959666 /note="CpG island score = 0.74, GC = 63.20%, CpGs = 25; Region: CpG island"		<pre>/evidence=not experimental 77947905 /note="GRAIL, score = 52.000%, comment = good"</pre>	<pre>/rpt_tamily="AluJo" complement(77337878) /note="GRAIL, score = 57.000%, comment = good shadow"</pre>			<pre>/note="GRAIL, score = 56.000%, comment = good" /evidence=not_experimental 43434367</pre>	<pre>/note="GenScan, score = 1.75*, comment = Initial_exon 129 bp frame: 0 phase: 0" /evidence=not_experimental complement(38473975)</pre>	

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hes 119;
L Submitted (17-NoV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Green, 320 Charles Street, Cambridge, MA 02141, USA 1 bases 1 to 158049)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pietre, N., Hafez, N., Hagos, B., Hortcon, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Steaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Baldwin, J., Barra, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
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Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Noy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Teefaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Direct Submission
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/gene="Mouse homologue of the human APECED gene
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AC138672

Mus musculus chromosome 10 clon
SEQUENCE, 13 unordered pieces.
AC138672
AC138672.3 GI:29150492
HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)

Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                          CGCTCCGGGAGATCCCCAG
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Center clone name: 522_L_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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5: gap of 100 bp
3: contig of 16858 bp in length
7: gap of 100 bp
7: gap of 100 bp in length
7: gap of 100 bp
5: contig of 2414 bp in length
5: gap of 100 bp
5: contig of 28878 bp in length
5: gap of 100 bp
2: contig of 36517 bp in length
2: gap of 100 bp
3: contig of 14207 bp in length
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Pred. No. 5.2e-09;
                                                                                                                                     190019 bp
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                                                                                                                     clone RP23-411J14 map 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL Submitted (15-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (Dases 1 to 190019)

Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boyuslawkiy, L., Boukhgalter, B., Comarata, J., Chang, J., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Mendirim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., Stubbs, M., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Stange-Thomann, N., Stubbs, M., Stubs, M., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2003 this sequence replaced gi:28394987. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Nusbaum, C.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                        Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 186501 bases at least Q30 Consensus quality: 18757 bases at least Q30 Consensus quality; 188318 bases at least Q30
                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                                                                                                                                                                                                                                                                        Center clone name: 411 J
                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
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in Q20 bases; sum-of-contigs
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167104: contig of 26336 bp
167204: gap of 100 bp
190019: contig of 22815 bp
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gap of 100 bp
contig of 3106 bp in length
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of 2227 bp in length
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AC108592/c
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Allen,C., Allen,H., Alsbrooke,S., Amin,A., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooke,S., Amin,A., Anguiano,D., Anyalabechi, W., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burchl,H., Calderon,E., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chen,Z., C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC108592
AC108592.5 GI:25006698
HTG: HTGS_PHASE1; HTGS_DRAFT; Rattus norvegicus (Norway rat)
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Pred. No. 5.1e-09;
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23270241.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents as scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 217688)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 217688) Worley, K.C.
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shotgun sequence only contigs will be indicated in the feature
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

TITLE JOURNAL

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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 9 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                          as soon as it is available be preserved.
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Center clone name: CH230-144C19

Center clone name: CH230-144C19

Center clone name: CH230-144C19

Assembly program: Phrap; version 0.990329

Consensus quality: 177651 bases at least Q40

Consensus quality: 182606 bases at least Q20

Consensus quality: 185802 bases at least Q20

Estimated insert size: 178707; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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177790
177890
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161781
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Center code: BCM
Web site: http://
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211301
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0: contig of 161680 bp in length
0: gap of unknown length
9: contig of 9109 bp in length
9: gap of unknown length
9: contig of 6800 bp in length
9: gap of unknown length
1: contig of 11792 bp in length
1: gap of unknown length
1: gap of unknown length
0: contig of 21519 bp in length
0: contig of 1389 bp in length
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SOURCE
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Muzny, D. Marie:, Metzker, M. Lee:, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooka, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Cookrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
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AC109383.5 GI:25006726
HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Rattus norvegicus clone CH230-48B22,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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87246. .89004
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189782. .190939
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71480. .74410
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10093. .11330
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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177890. .179119
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175878. .177789
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|70990. .172417
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214330: contig of 1441 bp in length
214430: gap of unknown length
215739: contig of 1309 bp in length
215839: gap of unknown length
217688: contig of 1849 bp in length.
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.161680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 90.2; DB 2;
Pred. No. 8.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear HTG 15-NOV-2002
SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 217688;
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Center project name: GPWN Center clone name: CH230-

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Project Information

Center code: BCM

```
Egan, A., Becctto, M., Bugene, C., Evans, C.A., Falle, T., Fan, G., Ferrandez, S., Finley, M., Falgey, M., Fortes, M., Foster, P., Fraser, C.M., Gabisi, A., Gante, R., Garcia, A., Garner, M., Glevera, W., Ghrist, A., Garrier, M., Glevera, W., Ghrist, A., Garrier, M., Glevera, W., Ghrist, M., Garrier, M., Glevera, W., Garrier, M., Grennandez, J., Harrier, M., Ghrist, M., Hamilton, M., C., Hamilton, K., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C., Kovar, G., Kraft, C.L., Lebow, H., Levan, J., Leva
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RESULT 42
BV163805
                    KEYWORDS
SOURCE
                                                             VERSION
                                                                             ACCESSION
                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
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Best Local S
Matches 101
  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                        23049
                                                                                                                                                                                                                                                                                                                                                      101;
                    BV163805.1 GI:47270013
STS.
Mus musculus (house mou
                                                                           tagged site.
BV163805
                                                                                                                    BV163805 558
RPAMMSEQ0036732 Roche Palo Al
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 5 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.
                                                                                                                                                                                                                                                                        GGCTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGCAGATCCCCAG
                                                                                                                                                                                                                                                                                                                 CAGAAGAACGAGGATGAATGCGCTGTGTGCCATGACGGAGGCGAGCTCATCTGCTGAC 23048
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93016
93116
162411
162511
281692
281792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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/note="clone_boundary
clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_end_extension clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end_sequence:BH362533"
88940. .90031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="CH230-48B22"
803. .35510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="wgs_end_extension clone_end:Sp6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="clone_boundary"
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17197: gap of unknown length
93015: contig of 75818 bp in length
93115: gap of unknown length
162410: contig of 69295 bp in length
162510: gap of unknown length
281691: contig of 119181 bp in length
281791: gap of unknown length
283951: contig of 2160 bp in length.
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                    (house mouse)
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Pred. No. 8.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                    58 bp
                                                                                                                    Mus
                                                                                                                                      DNA
                                                                                                                    musculus
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                                                                                                                                    linear
                                                                                                                STS genomic, sequence
                                                                                                                                    STS 15-MAY-2004
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Primer A: No primer submitted

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STS
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ORGANISM
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BV089350
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                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                            AUTHORS
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                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 574)

Nonven.A. Bach,C., Puech,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usuka, J., Liao, G., Cheng, J., McPherson, J.D., Foernzler, D. Mus musculus SNPs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                   tagged site.
BV089350
                                                                                                                                                                                                                                                                                                                                                    BV089350 574 bp
RPAMMSEQ0001246 Roche Palo Alto
                                                   Contact: Jonathan Usuka
Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
                                                                                                                                       Usuka,J., Liao,G., Cheng,J.,
McPherson,J.D., Foernzler,D.
Mus musculus SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
3431 Hillview Ave, Mailstop S3-1, Palo Alto, CA:
Tel: 6508555807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 558)
                Tel: 6508555807
                                3431 Hillview Ave, Mailstop S3-1,
                                                                                                                       Unpublished (2003)
                                                                                                                                                                                                                                                                                                   BV089350.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer A: No primer submitted with this Primer B: No primer submitted with this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Jonathan Usuka
                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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Jonathan.Usuka@roche.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jonathan. Usuka@roche.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="10-7927-7476-CAAA01111727.1.1.11206"
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/note="Sups developed from assay sequences derived from 15
/note="Sups developed from assay sequences derived from 15
different strains of mice (as of October 1, 2003). Those
strains include A/J, A/HeJ, 129/Sv, AKR/J, B10.D2-H2/OSnJ,
BALB/CB/J, BALB/CJ, C3H/HeJ, CSTPL/GJ, CAST/Ei, DBA/2J,
MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                   GI:37666829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 82.6; DB 11;
Pred. No. 7e-06;
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                                                                                                                                                         Nguyen, A., E
and Peltz, G.
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and Peltz, G.
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                                    Palo
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                                                                                                                                                                                                                                                                                                                                                        musculus
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                                  Alto, CA 94024,
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us STS ç
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STS
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ORIGIN
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BV088992
LOCUS
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AUTHORS
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Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 593)
Usuka,J., Liao,G., Cheng,J., Nguyen,A., Bach,C., Puech,A., McPherson,J.D., Foernzler,D. and Peltz,G.
Mus musculus SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 bp
RPAMMSEQ0000888 Roche Palo Alto
                                                                                                                                                                                                                                   Email: Jonathan.Usuka@roche.com
Primer A: No primer submitted
Primer B: No primer submitted.
                                                                                                                                                                                                                                                                                                                     Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
                                                                                                                                                                                                                                                                                                                                                      Contact: Jonathan Usuka
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BV088992.1 GI:37666471
                                                                                                                                                                                                                                                                                                   3431 Hillview Ave, Mailstop S3-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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/clone lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15
different strains-of mice (as of October 1, 2003). "Those
strains include A/J, A/HeJ, -229/Sv, AKRJ, B10.D2-H2/OSnJ,
BALB/CByJ, BALB/CJ, C3H/HeJ, C57BL/6J,-CAST/Ei, DBA/2J,
NRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15
different strains-of mice (as of October 1, 2003). Those
strains include A/J, A/HeJ, -129/Sv, AKR/J, B10.D2-H2/cSnJ,
BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J,-CAST/Ei, DBA/2J,
MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.-"
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/db_xref="taxon:10090"
/map="10-7927-7476-CAAA01111727.1.1.11206"
                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                     ocation/Qualifiers
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Pred. No. 7e-06;
0; Mismatches 29;
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Query Match
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Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A Potter, N.T., Ross, C.A. and Margolis, R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens junctophilin 3 (JPH3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (05-OCT-2001) Psychiatry, Institutions, 600 N. Wolfe St., Balt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 125020)
Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                  /gene="JPH3"
/product="junctophilin 3"
complement (<36507. .36887)</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                         complement (35581.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
                     /trānslation="mssggrfnfddggsycggwedgkaHgHgVcTgpkGQgeyTgSws
HgfEVLGVYTwpsgnTyQgTwaQgkRHGIGLESKGKWVYKGEWTHGfKGRYGVRECAG
                                                     /codon_start=1
/product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
/db_xref="GI:17646245"
                                                                                                                                                     membrane and endoplasmic
                                                                                                                                                                                                                                                                                        /note="synonym: JP3"
complement(<36507. .>36887)
                                                                                                                                                                                                                                                                                                                                                     /rpt_unit="ctg"
complement(<36507. .>36887)
NGAKYEGTWSNGLQDGYGTETYSDG"
                                                                                                                                                   /note="component of the junctional complex between plasmanembrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                  /gene="JPH3"
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                                                                                                                                                                                               gene="JPH3"
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AF429315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMKGGYMRYMRCWSMKRRWWGKSAMYRMRRWWKGRGAMMWCMKCYSRMSRCMMMKSYCA 17478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSCYKSYYMMARSKRMKGMKWGRCWGSMWGSASRSSCYKCYKSMRCSMMSSKCYRCAGCM 17418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTG
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                                                                                        SSMSCTSMYRCCWGGMKSYSTCGTTCKKCTGYKKSRTWYWWMYSWTSKMYMWR 1783:
                                                                                                                                                                                                TTTCTGGGGACACCAGCCATCATGTGCCTGGAAATTAAACCCTGCCCCACTTCTCTACTC
                                                                                                                                                                                                                                    KSASRSSWCSRRMKGMRGSCWSSKMWGGSRSRSASSKCKGSRGMRRRSKRSSKYRKRGRG
                                                                                                                                                                                                                                                                      TGGGATCAAGAAGGGGACAGCGCCACCTCTTGTCAGTGCTCGGCTGTAAACAGCTCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTAC
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                                                                                                                                                              KKRSMTKSKGSKGKSKCWKRSGSMTSSCYYYSASSCMWMMSSKSCMCCCMMMKRRCACCY
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                                                                                                                         TGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAATATAAAAA 1538
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Match 4.8%; Score 73.6; DB 9; Local Similarity 11.3%; Pred. No. 0.00016;
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                                                                                                                                                                                                                                                                                                                                                                                     209 GGCCCCACTGCCCTGTGAGGAAGGGTTCATGTGGTTGGTGTACAGTTCCGGGGCCCCTGG
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Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A Potter,N.T., Ross,C.A. and Margolis,R.L. A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 Nat. Genet. 29 (4), 377-378 (2001)
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Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
Direct Submission
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AF429315
WGSCYKCMKYYSGWSSYSTSMGYYSSTSCKKYKCSWSSMYKCKTSKSYRRKRSYYYWGGG
                                                 GCATGGGAGCAGGGCAGAGACTGGGGAGTTCAGGTACCCAGAGATGCTGCTGGGGGAGCT 447
                                                                                                                                                                                                                                                                      AACGCAGCAGCCTGCAAGAAACCGGGTTTTCTTCCCAATAGGGATGGCCCCGGGGGGTGT
                                                                                                      SYMWGMSMCMSCMSMAKSYMMCYCYMYRMSSYMSYYYKCYSCMGMSSTSYSYSCCWKMSS
                                                                                                                                                          CTGTTCGAGACÇAG-ATGGATGGGGAACAGGTGGTCAGGGCAGAATTTCAGGCCCTGGCA 387
                                                                                                                                                                                                                     ASRSMKCCWGGYRKSAGSKSSRGGTGYYMKKKGGGKGSMSSKKWKGSSTSRRRGSSAKSC
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/map="16924.3; between D16S520 and WI-12410"
/mote="160lated from a patient with Huntington's Disease-Like 2 (HDL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
/translation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGVCTGFKGQGEYTGSWS
HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWYYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
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complement(<36507. .>36887)
/gene="JPH3"
/product="junctophilin 3"
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/gene="JPH3"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/rpt_unit="ctg"
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Submitted (11-FBB-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: clonerequestas.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 11, 2004 this sequence version replaced gi:42517008.
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (bases 1 to 184594)
                                                                                                                                                                                                                                            Danio rerio (zebrafish)
Danio rerio
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Zebrafish DNA sequence from clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMSYSKCYSRWMWCMSYYYCWGGKCWSSCWWSSMRKKSKGGSWAKGMVWDKGSVSTDKSD 16908
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Sugiyama,T.,
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Mammalia; Eutheria;
                                                                                                                           Homo sapiens
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with miss sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one-plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: _EMBL; SwijSSPROT; Tr: _TREMBL; Wp:, WORMPED; Information on the WORMPED database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the submitted state of the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 AGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACG
          Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H. Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A.,
                                                                                                                                                                                                     AK127046.1 GI:34533779 oligo capping; fis (full insert Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                AK127046 AK127046 DP MRNA linear I Homo sapiens cDNA FLJ45103 fis, clone BRAWH3032571, n similar to Chromodomain helicase-DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and the beginning 'drr' were identified by Rick Waterman (Stephen Johnso lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-261L2
is from a Zebrafish BAC library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGTCCTCGTGCCTTTCATCTCTCTCTGTTGTGCCCCCCTCACCTCCATACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCACAATGATGATGAGTGTGCAGTGTAAAAGACGGCGGCGAGCTCATCTGCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-261L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="DKK1-2014"
/clone_lib="DanioKey"
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74.6%;
                                                                                                         Chordata;
Primates;
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Pred. No. 0.00077;
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                                                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                       sequence)
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                                                                                                            Hominidae;
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Inagaki,H.,
a., Ishii,S.,
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                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                        moderately
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                      1088 GGGCCTACCATCTCGTATGCCTGGACCCAGAGCTGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                  1028
                                                                                                                                            592 GGGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATCCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                   532 AGGACGAGTGTGCCGTGTGTCCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
652 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAG 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Pax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy. Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center to.); National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yemamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fuji, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Isogai, T. and Yamamoto, J.
                                                                                                                                                                                                              AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAGATCATCCTGTGCGACACCCTGCCCGA 1087
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDGYETDHQDYCEVCQQGGEIILCDTCPRAYHLVCLDPELEKAPEGKWSCPHCEKEGI
QWEPKDDDDEEEEGGCEEEEDDHWEFCRVCKOGGELLCCDACESSYHLHCLNPELPEI
PNGEWLCPRCTCPPLKGKVQRILHWRWTEPPAPFNVGLEGDDVEPSLPPPKPLEGIPE
REFFVKWAGLSYWHCSWYKELQLELYHTVMYRNYQRKNDMEPPPEPDYSGDEDGKSE
KRKNKDPLYAKMEEF FYRYGIKPEMMMIHRILMHSFDKKGDVHYLIKWKDLPYDQCTW
BIDDID PYYDNLKQAYWGHRELMLGEDTGLPKRLLKKGKKLADDKQEKPPTPIVDP
TVKFDXQPWYIDSTGGTLHPYQLEGLNWLRESWAQGTDTIADEMGLGKTVQTIVFLY
SLYKEGHSKGFYLVABLSTIINWEREFEMMAPDFYVVTYTGIKESRSVIRENBEFSFE
DNAIRSGKVFRMKKEVQIKFHVLLTSYELITIDQAILGSIEMACLVVDEAHRLKNNQ
SKFFRUNNSYKLDYKLLLTGTPLQNNLEEELFHLLNFLIPERFWLLEGFLEEFADISK
SKFFRUNNSYKLDYKLLLTGTPLQNNLEEELFHLLNFLIPERFWLLGGFLEEFADISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKDKKEKAKRKKKDEDEDDNDDGCLKEPKSSGQLMAEWGLDDVDYLFSEEDYHTLTN
YKAFSGPLRPLIAKKUPKI PMSKMMTVLGKWREPSANNPFKEXBAAAAAAVAAAVE
TVT1SPENAVSPPQVPPQVPI IKAKTKEGKGPGVRKKIKGSKDGKKKKKKKTAGLKF
RFGGISNKRKKGSSSEEDEREESDFDSASIHSASVRSECSAALGKKSKRRRKKKRIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSLPKKKKPKKLKENKCKGKRKKKEGSNDELSENEEDLEEKSESEGSDYSPNKKKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATWMRKTPGHRSQGSPWKSRPFQPPWIEWRVRTSTRAQPARREPERSGQRRRRRPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQIKKLHDLLGPHMLRRLKADVFKNMPAKTELIVRVELSQMQKKYYKFILTRNFEALN
SKGGGNQVSLLNIMMDLKKCCNHPYLFPVAAVEAPVLPNGSYDGSSLVKSSGKLMLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGAQQFCF1LSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQTKWKPSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KMLKKLRDEGHRVLIFSQMTKMLDLLEDFLEYEGYKYERIDGGITGGLRQEAIDRFNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MRGPVGTEEELPRLFAEEMENEDEMSEEEDGGLEAFDDFFPVEP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAC86802.1"
/db_xref="GI:34533780"
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/clone_lib="BRAWH3"
/note="cloning vector: pME18SFL3"
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'db_xref="taxon:9606"
'clone="BRAWH3032571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1/
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                                                                                                                                                                                                                                                                                                                                                                                    4.2%;
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                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 9;
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                       60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4966;
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SOURCE
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AF425231
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Homo sapiens chromodomain helicase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thompson, P.M., Gotoh, T., White, P.S. and Brodeur, G.M. CHD5, a New Member of the Chromodomain Gene Family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thompson, P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preferentially Expressed in the Nervous System
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DNAIRSGKKVFRMKERVQIKFHVLLTSYELITIDALIGSIEMARCLVVDEAHRLKONG
SKFERVLNSYKIDYKLLTGTPLONNULEELFHLINFLTPERFANILGSLEMACLVVDEAHRLKONG
SKFERVLNSYKIDYKLLTGTPLONNULEELFHLINFLTPERFANILGSLEMACLFALIN
EQGIKKLHDLLGPHMLRRLKADVFKNMPAKTELIVRUELSQMQKKYYKFILTRNFEALN
SKGGGRQVSLLNIMMDLKKCCNHPYLFPVAAVEAPVLFNGSYDGSILVKSGKLMLLQ
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PGAQQFCFLLSTRAGGLGINLATADTVIIYDSDMNPHNDIQAFSRAHRIGQNKKVMIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDGYETDHQDYCEVCQQGGEIILCDTCPRAYHLVCLDPELEKAPEGKWSCPHCEKEGI
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PNGEWLCPRCTCPPLKGKVQRILHWRWTEPPAPFWVGLPGDDVEPSLPPPKPLEGIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKAFSQFLRPLIAKKNPKIPMSKMMTVLGAKWREFSANNPFKGSSAAAAAAAVAAAVE
TVTISPPLAVSPPQVPQPVPIRKAKTKEGKGPGVRKKIKGSKDGKKKGKGKKKTAGLKF
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                                                                                                            EKILRHHYEQQOEDLARNIGKGKR I RKQVNYNDASQEDQEWQDELSDNÖSEYS I GSED
EDEDFEER PEGQSGRRQSRRQLKSDRDKPLPPLLARVGGN I EVLGFNARQRKAFLNA I
MRWGMPPQDA FNSHWLVRDLRGKSEKEFRAYVSLFWRHLCEPGADGAET FADGVPREG
                                                                                                                                                                                                      RFVTRASVEERITQVAKRKMMLTHLVVRPGLGSKSGSMTKQELDDILKFGTEELFKDD
VEGMMSQGQRPVTPIPDVQSSKGGNLAASAKKKHGSTPPGDNKDVEDSSVIHYDDAAI
SKLLDRNQDATDDTELQNMNEYLSSFKVAQYVVREEDGVEEVEREIIKQEENVDPDYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFFVKMAGLSYMHCSWVKELQLELYHTVMYRNYQRKMDMDEPPFDYSGSDEDGKSE
KRKNKDPLYAKMEERFYRYGIKELMCAEDTRLÞKRLLKKGKKLHDLKGKEVEPDTPIVDF
EIDDIDIPYKDNLKQAYWGHRELMCAEDTRLÞKRLLKKGKKLHDDKQEKFPDTPIVDF
TVKFDKQÞWYIDSTGGTLHÞYQLEGLNWLRFSWAQGTDTILADEMGLGKTVQTIVFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSLPKKKKPKKLKENKCKGKRKKKEGSNDELSENEEDLEEKSESEGSDYSPNKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon start=1
/product="chromodomain helicase DNA binding protein
/protein id="AAL98962.1"
/db_xref="GI:19773960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                      SRQHVLTRIGVMSLVRKKVQEFEHVNGKYSTPDLIPEGPEGKKSGEVISSDPNTPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKDKKEKKAKRKKKDEDEDDNDDGCLKEPKSSGQLMAEWGLDDVDYLFSEEDYHTLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MRGPVGTEEELPRLFAEEMENEDEMSEEEDGGLEAFDDFFPVEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 map="1p36.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="CHD5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01. .5965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .9646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Children's Hospital of lvd., Philadelphia, PA 19104-4318,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA binding protein 5 (CHD5)
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REFERENCE
AUTHORS
TITLE
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COMMENT
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BC058578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusins, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Pahey, J., Helton, E., Ketteman, M., Wadan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC058578 6438 bp mRNA linear ROD 30 Mus musculus chromodomain helicase DNA binding protein 4, (CDNA clone MGC:68269 IMAGE:6489649), complete cds.
                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                    Submitted (22-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 6438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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BC058578.1 GI:35193270
                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                             Strausberg,R.
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                                                                                                                        Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                    12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | GGGCCTTCCACCTGGCCTGCCTGTCCCCCTCCGCGGGAGATCCCCAGTGGGACCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCCTACCATCTCGTATGCCTGGACCCAGAGCTGGAGAAGGCTCCCGAGGGCAAGTGGA 1247
                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 6438)
Sequencing by: Nation uencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (house mouse)
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SKESLAGNKPANAVLHKVLNQLEELLSDMKADVTRLPSMLSRIPPVAARLQMSERSIL
SRLTNRAGDPTIQQGAFGSSQMYSNNFGPNFRGPGPGGIVNYNQMPLGPYVTDI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.2%;
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Pred.
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No. 0.012;
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Gupte, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, B., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
found
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 127 Row: m Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF passed the following selection. Similarity but not identity analysis.
                                    protein.
ocation/Qualifiers
                                                                                 identity
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FEATURES

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source
YTPGKKKKKIGAGEKEKISK KKEKEEREEDEDDDSKEEKSSAQLLEDWGMED I DHVF
SEEDVETLTNYKAFSQEVRPLLAAKDEK IA VSKMMVLJAKWREESTNUE FKGSGAS
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DMEKAPEGKMSCPHCEKEGI QMEAKEDNSEGEE I LEEVGGDPEEDDHHMEFCRVCLDP
DMEKAPEGKMSCPHCEKEGI QMEAKEDNSEGEE I LEEVGGDPEEDDHHMEFCRVCLDP
DMEKAPEGKMSCPHCEKEGI PROEMERTEVRQQKOST VHICSWYSDLALL WKWGQPPS
PTPVPREPDADPNTES PKPLEGR PERQPFVKNQGMSYNHCSKYGKI LL WKWGQPPS
PTPVRREPDADPNTES PKPLEGR PERQPFVKNQGMSYNHCSKYGKI LL WKWGQPPS
PTPVRREPDADPNTES PKPLEGR PERQPFVKNQGMSYNHCSKYGKI LL WKWGQPPS
PTPVRREPDADPNTES PKPLEGR PERQPFVKNQGMSYNHCSKYSKI LL WKWGQPPS
PTPVRREPDADPNTES PKPLEGR PERQPFVKNQGMSYNHCSKYSKYTELI LUMS
VDKGHHYLL KRUDLFYDAAMESED PK TO LAWALLER PKWAP DMYVVT
YVGDKOSRAI I RENEFS FEDNAL RGGKKARSHKKEASVKFHVLLT SELLT I DWAI LG
SI DWACLI VDEAHRLKONQSKFFRVLNGYSLQHKLLL TGTPLQNNLEEL PHLLNPLTP
ERFHNLEGFLESFAD I AKEDQI IKKLHDMLGFHKRIKKCASYNFHVLLT SELLT I DWAI LG
SI DWACLI VDEAHRLKONQSKFFRVLNGYSLQHKULL TGTPLQNNLEEL PHLLNPLTP
ERFHNLEGFLESFAD I AKEDQI IKKLHDMLGFHKRIKKCCNHYPKLFPVLAMEAFBYNPN
GMYDGSALI RASGKLLLL QKMLKVILKEGGHR VLI FSQMTKMLDILED FLEHEGYKYER
I DGGI TONMGOEAI DRAEDQI TKLHDMLGFHKILL TADTVI I YOSDMNEHND
I DGGI TONMGOEAI DRAEDQI TKLHDMLGFHKILL TADTVI I YOSDMNEHND
I DGGI TONMGOEAI DRAEDQI TCHWESTARAFSIA PKYPN
GMYDGSALRI LGERGAGGEEDSWGEI I KQEESVOD DYWSKLLAHIYSCOQOE
DLANULGKGKRI KOVNYNOSGOEDDDDGSDONGOSDODDFDERSEBAPR
RPSRKGLRNDKDFL KAVONYNOSGOEDSWGDDDGDSDSTARDGAGGEDDDPDERSEBAPR
RPSRKGLRNDKDFL KAVONYNOSGOEDSWGDDDGDSDNGASTFDODUTNET DAVDD
LEKKOGEREHVNGEMANDEL SEVERNKWMGDCSSESSERTPTDGVERSGDDDDDERSEBAPAPADPD
LEKKOGEREHVNGEMANDEL SEVERNKMWGDCSSESSERTFTDGVERSGDDDDDGAGGEDDDDDGAGGEDDDDFDERSTADDAVDD
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EAETPKLKKKKCPKKPRDPKIPKSKRQKKELGDSSGEGPEFVEEEEEVALRSDSEGSD
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/tissue type="bye, retina, mouse strain C57Bl\6"
/clone_Tib="NIH_MGC_94"
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/db_xref="LocusID:107932"
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/protein_id="AAH58578.1"
/db_xref="GI:35193271"
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IRKKVQEFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQPNTPAPVPP AEDGIKIEENSLKEEBSTEGEKEVKSTAPEATVECAQPPAPATATAPATATAPEDDKA PAEPPEGEEKVEKAEVKERTEEPMETEAKGTTEVEKVEEKSAVDLTPIVVEDKEEKKE

BEEKKDVMLQNGETPKDLSDEKQKKNSKQRFMFNI ADGGFTBLHSLWQNEERAATVTK

gg

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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Riserren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Brown, A., Campopiano, A., Chang, J., Chazaro, B., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farorson, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Gand-pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Gand-pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Lindblad-Toh, K., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Lind, G., MacCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stemann, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Volley, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1563 TTCCTACCACATCCACTGCCTGAACCCCCCCGCTGCCAGAGATCCCCAAACGGCGAATGGCT 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1503 GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGAGCTCCTGTGCTGACACATGCCCTTC 1562
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Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 67573)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
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Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,
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Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus clone RP24-489C24, LOW-PASS SEQUENCE SAMPLING.
AC122760
AC122760.2 GI:21427758
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Birren, B., Linton, L., Nusbaum, C. and Lander, B.
                                                                                                                                                                                                                                                                            Submitted (25-MAY-2002) Whitehead Institute/MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus, clone RP24-489C24
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Pred. No. 0.028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 15, 2002 this sequence version replaced gi:21206372. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             will be sequenced to completion. In the event
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
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REFERENCE AUTHORS

REFERENCE

AUTHORS

JOURNAL

Unpublished

(bases 1 to 67573)

TITLE

REFERENCE

TITLE

JOURNAL

KEYWORDS SOURCE ORGANISM

Mus musculus Mus musculus (ho

musculus (house mouse)

DEFINITION ACCESSION VERSION

RESULT 51 AC122760

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ORIGIN

Query Match Best Local

Matches

89;

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653 GTGCTCCAGCTG 664

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1623

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Gaps

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19336: gap of 100 bp
20142: gap of 100 bp
20160: gap of 100 bp
21760: gap of 100 bp
22575: gap of 100 bp
23281: gap of 100 bp
23281: gap of 100 bp
24898: contig of 701 b
24898: contig of 691 b
25789: gap of 100 bp
25689: contig of 691 b
25789: gap of 100 bp
26881: gap of 100 bp
27288: contig of 689 b
27288: contig of 689 b
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Center: Washington University Genome Sequencing of Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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On Mar 5, 2003 this sequence version replaced gi:28626883
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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McPherson,J.D. and Waterston,R.H.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)
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AC134529
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NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                               Usuka, J., Liao, G., Cheng, J., McPherson, J.D., Foernzler, D. Mus musculus SNPs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                      tagged site.
BV089378
BV089378.1 GI:37666857
                                                    Contact: Jonathan Usuka
Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
3431 Hillyiew Ave, Mailstop S3-1, Palo Alto, CA (
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 572)
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RPAMMSEQ0001274 Roche Palo Alto Mus
                                                                                                                                                                                                                                                                                   Mus musculus
Email: Jonathan.Usuka@roche.com
Primer A: No primer submitted
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                                      6508555807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1201
1301
6881
6981
38528
38628
93611
93711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig28" 38628. .93610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig29" 93711. .173909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6981. .38527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_name:Contig27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP24-503A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic una
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Q
1. .173909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_name:Contig30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_name:Contig22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1200: contig of 1200 bp in length
1300: gap of unknown length
6880: contig of 5580 bp in length
6980: gap of unknown length
38527: contig of 31547 bp in length
38627: gap of unknown length
93610: contig of 54983 bp in length
93710: gap of unknown length
173909: contig of 80199 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63.2; DB:
Pred. No. 0.016;
                                                                                                                                                                                    Nguyen, A., Bach, C., Puech, A., and Peltz, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the accession number will
                                                        Palo Alto, CA 94024, USA
                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 173909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                            linear STS 19 se STS genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                STS 15-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        652
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 54
AC097256/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                     RS Muzny, D. Marie .. Metker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Bardaranaike, D., Barber, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Conter, R., Center, A., Crotee, A., D'Souza, L., Cardenas, V., Chen, Z., Chu, J., Chen, Z., Chu, J., Check, A., D., Chen, Z., Chu, J., Chacko, J., Cokrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Depar, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Pernandez, S., Finley, M., Flaggy, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gharata, P., Hadun, S.L., Hodgson, A., Hernandez, J., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Jackson, A., Jac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 TCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC097256 248835
Rattus norvegicus clone CH230
***, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer B: No primer submitted 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC097256
AC097256.6 GI:30521113
                                       Milosavljevic,A., Miner,G., Minja,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAGCCTGAGGTGTCCAGGCCCCCGGAGCNACCTGCAGAGACCCCGGTATGCCC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCGGGCAGAGGAGCCCCGGCCCCAAGGAGCCCACCGTGGAGACCCCGGTCCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACACAGTGGCCTCTGGAGATGCTCCTGCTGCCTCCAGGGCAGAGTCCAACAGAACCTGT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 248835)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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/note="SNPs developed from assay sequences derived from 15
different strains-of mice (as of October 1, 2003). Those
strains include A/J, A/HeJ, -129/Sv, AKR/J, B10.D2-H2/oSnJ,
BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J,-CAST/Ei, DBA/2J,
MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.~"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="taxon:10090"
/map="10-9361-9932-CAAA01111727.1.1.11206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.1%;
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Pred. No. 0.05
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48835 bp D
CH230-172E6,
a,E., Montemayor,J., Moore,S.,
Munidasa,M., Murphy,M., Nair,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6, ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG 10-MAY-2003
IN PROGRESS
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:23100986.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunasgoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovio,D., Primus,E., Pu,L.-L.,
Plopper,F., Poindexter,A., Popovio,D., Primus,E., Pu,L.-L.,
Plopper,F., Poindexter,A., Popovio,D., Primus,E., Pu,L.-L.,
Plopper,F., Poindexter,A., Rose,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuver,M., Richards,S., Riggs,F.,
Reilly,B., Reilly,M., Ren,Y., Revers,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sison,I., Sitter,C.D., Smajs,D.,
Sned,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Sned,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasna,D., Walter,B., Wang,J.,
Wang,O., Wang,S., Warren,R., Wei,X., White,F.,
Wang,O., Wang,S., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Warjaht,R., Wu,J., Yakub,S., Yen,J., Yoon,L.,
Yu,F., Zhang,J., Zhou,J., Zhou,J., Zhou,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Peinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 248835)
                                                                                                             * NOTE: Betimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/doce/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission
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                                       as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- Genome Center
23011: contig of 23011 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           College of Medicine
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COMMENT

REFERENCE TITLE JOURNAL

AUTHORS

TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

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AC127615
LOCUS
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KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127831 TTCCTACCACATCCACTGTCTGAACCCCCCACTGCCCGACATCCCCAATGGTGAATGGCT 127772
              Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Ballen, C., Allen, H., Ayodeji, M., Baca, E., Baden, H., Ballewin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brawlon, K., Blyth, P., Burstead, M., Benahmed, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Celderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Dary-Carroll, L., De Anda, C., Dederich, D., Davila, M. L., Davis, C., Dary-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Danson, S., Deramo, C., Dinh, H., Divya, K., Deramo, C., Ding, Y., Dinh, H., Divya, K., Drager, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganria, R., Garreia, M., Guerra, W., Guevara, W., Gebregoorgis, E., Geet, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Guerra, W., Guevara, W., Harvey, Y., Havels, S., Haddun, S.L., Hodgson, A., Hogues, M., Hernandez, J., Hanes, S., Haldun, S.L., Hodgson, R., Johnson, R., Joltest, A., Hollins, B., Howells, S., Haldun, S.L., Hong, J., Jackson, A., Hollins, R., Johnson, R., Joltest, A., Hollivet, A., Hollins, R., Johnson, R., Joltest, A., Hollivet, A., Lackson, L., Jackson, A., Hollivet, A., Lackson, A., Hollins, R., Johnson, R., Joltest, A., Hollivet, A., Lackson, L., Jackson, J., Hanes, J., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC127615.3 GI:25086972
HTG; HTGS-PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus clone
AC127615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCTTCCACCTGGCCTGCCCTGCCCTCCGGGAGATCCCCCAGTGGGACCTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCCAGGAGCCACCCGTGGAGACCCCGCTCCCCC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCCCTCGATGCACGGTAAGTAGAACCTCATCCTCACAGCGCCCACCATCCAAGCGCCA 127712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 273874)
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247146
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244670: contig of 221559 bg in length
244770: gap of unknown length
245826: contig of 1056 bg in length
245926: gap of unknown length
247145: contig of 1219 bg in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247245: gap of unknown
248835: contig of 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0%; Score 61.4; DB 2; Length 248835; 55.3%; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Qualifiers
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1e CH230-28C23,
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WORKING DRAFT SEQUENCE.
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Idlebird, D., Jackson, A., Johnson, R., Jolivet, A.,
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Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Louleeged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Maheshwari, M., Mahindartne, M., Martin, R., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Martiney, S., McLeod, M. P., Koeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Minja, E., Montemayor, J., Moore, S., Minja, E., Montemayor, J., Mark, K., Parks, K., Pathervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nahervis, C., Pall, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul.-L., Posterrak, S., Rejger, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Snetty, J., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shethy, J., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Vallasana, D., Waldron, L., Walker, B., Wang, J., Warren, J., Warren, R., Wei, X., White, F., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Wallasana, D., Yon, Yu, F., Zhang, J., Zhou, J., Yoon, L., Non, J., No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23265433.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
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3 (bases 1 to 273874)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                               Center project name: GXLZ
Center clone name: CH230-28C23
Center clone name: CH230-28C23
Center clone name: CH230-28C23
Assembly program: Phrap; version 0.990329
Consensus quality: 230595 bases at least Q40
Consensus quality: 230595 bases at least Q30
Consensus quality: 232954 bases at least Q20
Consensus quality: 234439 bases at least Q20
Estimated insert size: 234885; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- Genome Center
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TITLE
JOURNAL
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AUTHORS
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JOURNAL

REFERENCE AUTHORS TITLE

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COMMENT

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TITLE JOURNAL

Direct Submission

Submitted (09-JUN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                            RESULT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                           ORGANISM
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4.0%;
Local Similarity 55.3%;
hes 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218661 TTCCTACCACATCCACTGTCTGAACCCCCCACTGCCCGACATCCCCAATGGTGAATGGCT 218720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218601
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 121375)
                                                                                                         Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                  complete sequence BX004850
                                                                                                                                                                                                                                         BX004850 121375 bp DNA linear VRT 10-JUN-200 Zebrafish DNA sequence from clone CH211-51M24 in linkage group 19,
Harrison, E
                                                                                                                                                                              BX004850.11 GI:48596641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCTTCCACCTGGCCTGCCTCCCGCTCCGGGAGATCCCCCAGTGGGACCTGGAG
                                                                                                                                                                                                                                                                                                                                                                            CCTTTCAGCCATTTCTGAGGCCGCGCAGCTCTTCC 218815
                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCCAGGAGCCACCCGTGGAGACCCCGCTCCCCC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCCCTCGATGCACGGTAAGTAGAACCTCATCCTCACAGCGCCCACCATCCAAGCGCCA 21878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by the finished sequence as soon as it is available the accession number will be preserved.

1 273874: contig of 273874 bp in length.
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clone_end:Sp6"
complement(2215..216348)
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complement(271364. .272156)
/note="clone_boundary
clone_end:T7
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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CQ541728
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an altempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em. EMBL; Swy. SWYSSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish puc subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71538
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                                                                                                                                  Sequence
CQ541728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-51M24 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jun 10, 2004 this sequence version replaced gi:37650840.
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                         Homo sapiens (human)
Eukaryota; Metazoa;.Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                        CQ541728.1 GI:41507992
                                                                                                                                                                                          CQ541728
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                                                                                                                                                           11363 from Patent
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/db_xref="taxon:7955"
/clone="CH211-51M24"
/clone_lib="CHORI-211"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seelig, H.P. and Renz, M.
DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
PATENT: WO 9628547-A 1 19-SEP-1996;
PRIVATES INST FUER IMMUNOLOGIE (DE)
Other publication DE 19509279 960515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
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Conservative (
                                                                                                                                                              /translation="AGGIGS PSPCSAGSEEBDMDALLUNSLPPPHPENBEDPEDLSE
/translation="AGGIGS PSPCSAGSEEBDMDALLUNSLPPPHPENBEDPEDLSE
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DSEGSDYTPGKKKKKLGPKKEKSKSKKKEEEEDDDDDDSKEPKSSAQLLEDWGME
DIDHYFSEEDYRTLTNYKAFSQFVRFLLAAKNFKIAVSKMMYLGAKWRAEFSTNUPFK
GSSGASVAAAAAVAVVESNYTATEVAPPPPPVEVPIKKKKYMEGKGPNARRKPKG
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PRVPDAKKPKPKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSVSDGS
TSRSSRSKKLTTKKKKKGEEEVTAVDGYSTTDHQDVCEVCQQGGEIILCDTCPRAYH
MYCLDPDMEKAPEGKWSCPHCEKEGIQWEAKBDNSEGEEILEEVGGDLEEBDDHHMSF
CRVCKDGGBLLCCDTCPSSYHIHCLNPPLPEIPNGPMSYETOCHSWSECJLEHC
WGQPPSPTPVPRPDDADPNYPSPKPLEGFRERQFTVKQGMSYMFGSWSECJLEHC
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DMAILGSIDWACLIVDEAHRLKNNQSKFFEDNAIRGKASRWKEASYKFHVLLTSYELITI
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VRUELSPMOKKYYKYLITRNEFSEDNAIRGGGRACHASRWKENTERLEADVFKMMPSKTELIT

VRUELSPMOKKYYKYLITRNEFSEDNAIRGGGRACHASRWKENTERLEADVFKMMPSKTELIT

VRUELSPMOKKYYKYLITRNEFSEDNAIRGGGRACHASRWKENTERLEADVFKMMPSKTELIT

VRUELSPMOKKYYKYLITRNEFSEDNAIRGGGRACHASRWKENTERLEADVFKMMPSKTELIT

VRUELSPMOKKYYKYLITRNEFSEDNAIRGGGRACHASRWKENTERLEADVFKMMPSKTELIT

VRUELSPMOKKYYKYLITRNEFSEDNAIRGGGRACHASRWKENTERLEADVFKMMPSKTELIT

VRUELSPMOKENTER

VR
                                                        APKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGHRVLIPSQMTKMLDLLEDFLEHE
GYKYERIDGGITGNMRQEAIDRFNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSD
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KTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGEDSSVIHYDDKAIERLLDRNQD
ETEDTELQGMNEYLSSFKVAQYVVREEEMGEEEEVEREIIKQEESVDPDYWEKLLRHH
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/db_xref="taxon:32644"
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Dermatomyositis-specific auto-antigen
Patent: US 6440679-A 1 27-AUG-2002;

Location/Qualifiers
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Sequence 1 from patent US 6440679
AR224019
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                                                                                                                                                                                                                                                                            AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
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AFTTOMLVRDLÆKSEKEFKAYVSLFWAHLCEPGADGAETFADGVPREGLSRGHVLTR
IGVMSLIRKKVQEFEHVNGRMSMPELLAVEENKHSQPGSPSPKTPTPSTFGDTQPNT
PAPVPPAAEDGIKIESISLKÆEESSIEGEKEVKSTAPETALECTQAPAPASEDEKVVVEP
PEGEEKVEKAEVKELSELKEEESSIEGEKEVKSTAPETALECTQAPAPASEDEKVVVEP
PEGEEKVEKAEVKERTEEPMETEPKGAADVEKVEEKSAIDLTPIVVEDKEEKKEEEEK
KEVMLONGETPKOLNDEKQKKNIKQRFMFNIADGEFTELHSLKQMEERAATVTKKTYE
IMHRHIDYMLAGIINHGYAAWGDIQNDPKYALILNEPPKGEMMRGNFLLEIKNKFLARR
PKLLEQALVIEGULRRAYLNMSEDPSHPSMALNTRPAEVECLAESHGHLSKESMAGN
KPANAVLHKYLKGLEELLSDMKADVTRLPATIARIPPAVAVRLQMSERNILSRLANRAP
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/mol_type="genomic |
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AR367436.1
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Seelig,H.P. and Renz,M.
Dermatomyositis-specific auto-antigen
Patent: US 6339517-A 1 11-DEC-2001;
Location/Qualifiers
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Seelig, H.P. and Renz, M.
Dermatomyositis-specific auto-antigen
Patent: US 6500923-A 1 31-DEC-2002;
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ilarity 61.5%;
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/mol_type="genomic |
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Sequence 2747 from Patent WO0194629.
AX332238
                                                                                                                                                                                                                                                                                                                                                                  Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: WO 02068579-A 8343 06-SEP-2002; PE Corporation (NY) (ME)
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Homo sapiens
                                                                                                                                                                                                                                                                                              Avalon Pharmaceuticals (US)
Location/Qualifiers
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Mammalia; Eutheria; Primatea; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA 1317
                                 GGGCCTTCCACCTGGCCTGTCCCCTTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA 651
                                                                   AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
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                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-APR-1995) H.P. Seelig, Molecular, Genetics, Kriegsstrasse 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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1 (Dases 1 to 6417)

Seelig,H.P., Moosbrugger,I., Ehrfeld,H., Fink,T., Renz,M. and
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Homo sapiens (human)
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etetpklkkkkkpkkprdpkipkskrokkermllcrqlgdssgegpefveeeeevalr
sdsegsdytpgkkkkkklgpkkekkskskskrkeeeeedddddskepkssaqlledwgm
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/cell line=
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/brotein id="CAA60384.1"
/db_xref="GOA:Q14839"
/db_xref="Swiss-Prot:Q14839"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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9, D-76133 Karlsruhe, FRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1327 AĞĞACTATTĞCĞAĞĞTĞTĞCCAĞCAAĞĞĞTĞAĞATCATCCTĞTĞATACCTĞTCCCC 1386
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                                                                                                                                                                                                                                                                                                                                                                                                                                             592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
AR338834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 6475)
Tang,Y.T., Zhou,P. and Drmanac,R.T.
Nucleic acids and polypeptides
Patent: US 6569662-A 325 27-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                      BC038596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
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                                                                             domo sapiens chromodomain helicase DNA binding protein 4,
(cDNA_clone MGC:46187 IMAGE:5528023), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
                                                                                                                                                                                                                                                                                                                                                                                       GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC 1257
                                                                                                                                                                                                                                                                          GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCAGAGATCCCCAGTGGGACCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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TPAPVPPAEDGIKIERNSLKEERSIEGEKEVKSTAPETAIECTQAPAPASEDEKVVVE
PPEGEKVVPPAEDGIKIERNSLKEERSIEGEKEVKSTAPETAIECTQAPAPASEDEKVVVE
PPEGEKVEKALDLIP TVADKREKKEERE
PPEGEKVEKALDLEKOKRALDVEKVEEKALDLIP TVADKREKKEERE
KKEVMLQNGETPKOLNDEKQKKNIKQRRMFNIADGFTELHSLMQNEERAATVTKKTY
EIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEMNRGNFLEKKNKFULAR
RFKLLEQALVIEEQLRRAAYLNMSEDPSHPSMALNTRFAEVECLAESHQHLSKESMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 from patent
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1. .6475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAFTTQWLVRDLRGKSEKEFKAYVSLFMRHLCEPGADGAETFADGVPREGLSRQHVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.9%;
                                                                                                          6584 bp chromodomain helicase
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Pred. No. (
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Pred.
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                                                                                                                                   mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6417;
                                                                                                                                   linear
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                                                                                                                                   PRI 07-OCT-2003
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AUTHORS
                                                                                                                                                                                                                                                                                                                                FEATURES
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, B., Ketteman, M., Madan, A., Kodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,

Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.

Generation and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 78 Row: o Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Bletrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Idetrich,N.L., Granite,S., Guan,X., Gupta,J., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nc
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:46187_IMAGE:5528023"
/clone="MGC:46187_IMAGE:5528023"
                      gene="CHD4"
                                                   1. .6584
                                                                                                                              tissue type="Skin, melanotic melanoma."
(clone_lib="NIH_MGC_72"
                                                                                                                                                                                                                                                                                                       L. .6584
                                                                                note="Vector:
                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                            lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://mgc.nci.nih.gov
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S 밁 á 밁 Ś

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ORIGIN
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CLDPDMEKAPECKWSCPHCEKEGIQWEAAKEDNSEGELLEEVQGDLEEEDDHHMEFCR
VCKDGGELLCCDTCPSSYHIHCLINPPLPEIPNGEMLCPRCTCPALKGKVQKILLIKKWG
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MFRNYQRKUDHDEPPSGDFGGBEKSRKRKINDPKPAEMEERTYRYGIKPEMMIHRI
LNHS VDKKGHVHYLIKWRDLPYDQASWESEDVEIQYDLFKQSYMNHRELMRGEEGRP
GKKLKKVKLRKLER PETTTVDFTVKYERQPEYLDATGGTTLHPYQMEGLIMWLR FSWAQ
GTDTILADEMGLGKTVQTAVPLYSLYKEGHSKQPFLYSAPLSTIINWEREPEMMAPDM
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KMPNGWYDGSALITAGGGNQVSLLNVVNDLCKCCMHPYLFSYAMDDEXX
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GNSKGGELDDILKEGTSELFRUNGKCKERSULFPLLARVGGNI
EVLGFNARQRKAFLNAIMRYGMPPDAAFTSKAKEBEAFRRPSRKCLRNDKKKPLPPLLARVGGNI
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TAPETAIECTQAPAPASEDEKKVEBEEKKEWLANDKKKERSESIEGSESTARVGAADVEK
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VGEKSAIDLTBIVSKAERBAATVKGTYFTAHBERHYWLLAGIILAGIILAGIAANDOCKONUBRYA

CGGFFRINSLONDBINGAERAKEEBEKKENDLONDBEKAANDOLONDBYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PHD; Region: PHD-finger. PHD folds into an interleaved type of Zn-finger chelating 2 Zn ions in a similar manner to that of the RING and PYVE domains" /db xrefe"CDD:pfam00628"
              /gene="CHDA"
/note="HeDA; Region: Superfamily II DNA/RNA helicases, SNF2 family (Transcription / DNA replication, recombination, and repair)"
/db_xref="CDD:COG0553"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CHD4"
/note="PHD; Region: PHD-finger. PHD folds into an interleaved type of Zn-finger chelating 2 Zn ions in similar manner to that of the RING and FYVE domains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGGFTELHSLMQNEBRAATVTKKTYBIMHRRHDYMLLAGIINHGYARWQDIQNDRYA
ILNEPFKGEMNRGNFLEIKNKFLARRFKLLEQALVIEBQLRAAYINMSEDPSHSMA
LNTREAEVECLAESHOHLSKESNAGNKDANAVLHKVLKQLEELLSDMKADVTRLFATI
ARIPPVAVRLQMSERNILSRLANRAPEPTPQQVAQQQ"
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DHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVSKMMVLGAKWREFSTNNPFKGS
SGASVAAAAAAVAVVESMVTATEVAPPPPVEVPIRKAKTKEGKGPNARRKPKGSPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPDAKKPKPKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSVSDGSTS
                                                                                                                                                                                                                                                                         domain"
                                                                                                                                                                                                                                                                                                                                                                        /db_xref="CDD:smart00298"
2017. .2181
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/db_xref="MIM:603277"
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/db_xref="GI:24047226"
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/db_xref="MIM:603277"
163. .5976
                                                                                                                                                                                                                                                                                   /gene="CHD4"
/note="CHROMO; Region: Chromatin organization modifier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="CHROMO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="CHD4
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L504. .1641
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AUTHORS
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AL589792
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Best Local
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90999
91099
130107
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Assembly program: XGRP4; version 4.5
Sequencing vector: M13; M77815; 12% of reads
Sequencing vector: plasmid; L08752; 87% of reads
Chemistry: Dye-terminator ABI; 14% of reads
Chemistry: Dye-terminator Big Dye; 60% of reads
Chemistry: Dye-primer-ameraham; 24% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 131709 bases at least 030
Consensus quality: 131965 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1382 GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL589792 bp DNA linear HTG 10-JUL-2001 Homo sapiens chromosome 1 clone RP5-889P23 map p36.21-36.33, 4
                                                                                                                                                                                                                                                                                                                                                                              Insert size: 132292; sum-of-contigs
Insert size: 132129; 14.2% error; agarose-fp
Quality coverage: 11.37x in Q20 bases; sum-ocoverage: 11.69x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: dJ889P23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL589792.1 GI:13277194
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                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
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be preserved.
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3431:
90998:
91098:
130106:
130206:
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                                                                                                                               3331:
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contig of 3331 bp in gap of 100 bp; contig of 87567 bp is gap of 100 bp; contig of 39008 bp is gap of 100 bp
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Pred. No.
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RESULT 68
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JOURNAL
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                               Submitted (20-0UL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone request@sanger.ac.uk
On Jul 22, 2000 this sequence version replaced gi:9368784.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34084
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                   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166518 bp DNA linear PR:
Human DNA sequence from clone RP1-120G22 on chromosome
1p36.21-36.33, complete sequence.
AL031847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166518)
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                      feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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130207. .132592
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1. .132592
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/clone="RP5-889P23"
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/chromosome="1"
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/mol_type="genomic DNA"
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was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP1-120G22 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone RP1-120G22 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP1-20G22 is at 166518 in this sequence. The true left end of clone RP5-889P23 is at 90508 in this sequence. The true right end of clone RP1-20G08 is at 100 in this
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misc\_feature 94030 /note="match: GSS: Em:AQ097224"
complement(79470. .79747)
/note="match: STS: Em:AF191963" /note="Single clone region. short insert library only"
68250. .68620 /note="Single clone region. short insert library only"
complement(57981. .58764)
/note="match: GSS: Em:AF158011" /note="match: GSS: Em:AQ213363" complement (41123. .41505) /note="match: 94030. .94434 /note="match: 87339. .87808 complement (86963. complement (85942. complement (79935. complement(79556. .79740) /note="match: GSS: Em:AQ541496" complement (74554. complement (60582. 45297. .45591 complement (41087. .41505) /note="match: GSS: 25588. .26045 /note="match: GSS: Em:AQ239786" 10012. .10541 8816. .9229 /note="match: STS: /note="match: STS: Em:G21080" /note="match: STS: Em:G16281" 70460. .70622 49180. .49534 /note="match: /note="match: GSS: 18389. .18823 /mol\_type="genomic DN
/db\_xref="taxon:9606"
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RESULT 69
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Sequence 1
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/note="match: GSS: Em:AQ489599"
complement(113100. .113712)
/note="match: GSS: Em:AQ477048"
complement(113175. .113715)
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94054. 94464
/note="match: GSS: Em:AQ010380"
join(112106. .112211,116809. .116933,123047. .123132)
/note="match: GSS: Em:AQ634355"
complement (join(112121. .112215,116809. .116936))
/note="match: GSS: Em:AQ202845"
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/note="match: GSS:
152031 .152510
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complement(124491. .124832)
/note="match: STS: Em:G06939"
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complement(123035. 123248)
/note="match: GSS: Em:AQ779080"
123142. 123248
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/note="match: GSS: Em:AQ231956"
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join(116940. .116933,123047 .123191)
/note="match: STS: Em:G13224 Em:G13474"
/21507 .121762
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116809. .116936
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join(11609). 116933,123047. 123119)
/note="match: GSS: Em:AQ732842"
116809. 116941
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)oin(112145. .112211,116809. .116936)
note="match: GSS: Em:AQ634370"
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Pred. No. 0.07;
0; Mismatches
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Best Local Sim
Matches 103;
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                                                                                                                                                                                                                                                      Submitted (06-APR-1994) M. Bart Frank Foundation, Arthritis and Immunology Oklahoma City, OK 73104, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1591)

Ge, Q., Nilasena, D.S., O'Brien, C.A., Frank, M.B. and Targoff, I.N. Molecular analysis of a major antigenic region of the 240-kD protein of Mi-2 autoantigen

J. Clin. Invest. 96 (4), 1730-1737 (1995)
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Human Mi-2 autoantigen
U08379
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Targoff, I. N. and Ge, O.
The polymyositis and Patent: US 6610823-A 1 26-AUG-2003;
Location/Qualifiers
1. .1053
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Frank, M.B.
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                                                /note="Northern blot with this cDNA a single band in 7.5 kb region"
                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                  /cell_type="thymocyte"
/tissue_type="thymus"
/clone_Tib="thymocyte and
(Clontech)"
                                /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="unknown"
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partial cDNA encodes an antigenic region
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Pred. No. 0.17;
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                                                                                                                                                                                                                                                                                          Oklahoma Medical Research rogram, 825 NE 13th Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA, partial cds.
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Sequence 23239 from Pat
CQ491372
CQ491372.1 GI:41456991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 0160860-A 23239 23-AUG-2001;
Millennium Predictive Medicine, Inc. (U
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schlegel,R., Endege,W.O. and Monahan,J.E. Genes differentially expressed in human p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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GGTGCTCCAGCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA
                                                                         GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
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YHLVCLIDPELDRAPEGKMSCPHCEKBGVQWEALKEEEBDHMBY
CRVCKDGGELLCCDACIS YHHCEKBGVQWEALKEEBERF
CRVCKDGGELLCCDACIS YHHCEKBGVQWEALWEYECTCPVLKGRVQKILHMF
WGEPPVAVPAPQQADGNPDVPPPRPLQGRSEREFFVKWVGLSYMHCSWAKELQLEIFH
LUMYBNYQRKNDDBPPPLDYSGGEDDGKSDKRKVKDPHYAEMEEKYYRFGIKPEMMT
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                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="unassigned DN/
/db_xref="taxon:9606"
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RESULT 71 CQ491372 LOCUS

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KEYWORDS SOURCE ORGANISM

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ACCESSION
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TITLE
                              Query Match
Best Local Similarity
Matches 103; Conserv
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Best Local Similarity
Matches 103; Conserv
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532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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Sequence 30 from Patent
AX924076
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Sequence 29 from Patent
AX924075
                                                                                                                                                                                      Gene
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                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                             Homo sapiens
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                        1. .6331
                                                                                                         /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                   Location/Qualifiers
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Pred. No. 0.13
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AF006515
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ORGANISM
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Direct Submission
Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human Genome Research Institute, National Institutes of Health, 49
Convent Drive, Bethesda, MD 20892-4442, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6331)

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Characterization Sci. U.S.A. 94 (21), 11472-11477 (1997)
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                           AVAEQVSAAVSSATFIAPSGPPALPPPPAADIQPPPIRRAKTKEGKGPGHKRRSKSPR
VPDGRKKLRGKOMAPLKIKLGLLGGKRKGGSVYVGSDBGEPERBLESDLDSGSVHSA
SGRPDGPVRTKKLKGGBGKKKKKVLGCPAVAGBEEUDGYETDHODYCEVCQQGGEI
LCDTCPRAYHLVCLDPELDRAPBGKMSCPHCEKEGVQMEAKEEEEEYEEEGEEEGEKE
                                                                                                                                                                                                                                                                                                                                                 /trānslation="MKAADTVIIMARSKNDQLRISFPPGLCWGDRMPDKDDIRLLPSA
LGVKKKKRGPKKQKENKPGKPRKKKRDSEEEFGSERDEYREKSESGGSEYGTGPGRK
RRRKHBEKKEKYTKRRKKGEGDGGQKOKOVGKSSATILLTWGLEDVEHVFSEEEDYHTIVE
NYKAFSQFMRPLIAKKNPKIPMSKMMTILGAKWREFSANNPFKGSAAAVAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAB87383.1"
/db_xref="GI:2645433"
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/product="CHD3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="CHD3"
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mol_type="mRNA"
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LLRHHYEQQQEDLARNLGKGKRVRKQVNYNDAAQEDQDNQSEYSVGSEEEDEDFDERF
EGRRQSKRQLKNEKDKFLFPLLARVGGNI EVLGFWTRQRKAFLNAVMRWGWEPQDAFT
TQWLVRDLRGKTEKEFKAYVSLFMRHLCEPGADGSETFADGVPREGLSRQQVLTRIGV
MSLVKKKVQEFEHINGRWSMPELMFDDSADSKRSSRASSFTKTSFTTPEASATNSFC
SKPATFAPSEKGEGIRTPLEKZEAENQEEKPEKNSRIGEKMETEADAPSPAPSLGERL
                                                    QDIQNDAQFAIINEPFKTEANKGNFLEMKNKFLARRFKLLEQALVIEEQLRRAAYLNI
SQEPAHPAMALHARFAEAECLAESHQHLSKESLAGNKPANAVLHKVLNQLEELLSDMK
ADVTRLPATLSRIPPIAARLQMSERSILSRLASKGTEPHPTPAYPPGPYATPPGYGAA
                                                                                                                                                                                                                EPRKI PLEDEVPGVPGEMEPEPGYRGDREKSEDVKGDRELRPGPRDEPRSNGRREEKT
EKPREMENIADGGFTELHTLMQNEERAAISSGKLNEIMHRRHDYMLLAGIVLHGYARM
FSAAPVGALAAAGANYSQMPAGSFITAATNGPIHRFFKKVPEIQ"
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AX924049
LOCUS
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Best Local Similarity
Matches 103; Conserv
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1406
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                                                                                                                                                                                                                                                                                                                                                                                                                  Al-Mahmood, S., Colin, S. and Schneider, C.
Angiogenesis regulator genes, pharmaceutical preparations
containing same and uses thereof
patent: WO 03080105-A 3 02-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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AX924049
                                                                                                                                                                                                                                                                                                                                                                                                  Gene Signal (FR)
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                                                                                                      GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA 651
GCTGCCCTCACTGTGAGAAGGAGGGGGTCCAGTGGGAGGCCAAGGAAGAAGAAGA 1460
                                                                    GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCCAAATGGA
                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                 Length 6771;
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Homo sapiens zinc-finger helicase (hZFH) mRNA, complete cds.
U91543
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Aubry, F., Mattei, M.G. and Galibert, F.
Identification of a human 17p-located cDNA
the Snf2-like helicase family
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ERDDHMSYCRVCKOGGELLCCDACISSYHIHCLNPPLPDIPNEWLCPRCTCPVLKGR
VQKILHWRWGEPPAVPAPQADGNPDVPPPRPLQGRSEFFEYKWYGLSYWHCSWAK
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LEGLIWLRFSWAGGTDTILADEWGLGKTIQTIVFLYSLYKETQPRFITATGFTLYSAPLSTI
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VLLTSYELITIDQAALGSIRWACLVVDEAHRLKNQSKFFRVLNGYKIDHKLLKIGTP
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                                                                                                                     THLVVRPGLGSKAGSMSKÖELDDILKFGTEELFKDENEGENKEEDSSVIHYDNEAIAR
LLDRNQDATEDTDVQNNBYLSSFKVAQYVVREEDKIEZIEGENKEEDSPOTBY
LLRHHYEQQOEDLARNLGKGKRVRKKOVNYNDAAQEDQNQSYSVGSEEEDEDFDERF
EGRRQSKRQLRNEKDKPLFPLLARVGGNIEVLGFNTRQRKAFLNAVMRWGMPPQDAFT
TQWLVENDLRGKTEKEFKAYVSLFMRHLCEPGAAGSETFADGVPREGLSRQQVLTRIGV
MSLVKKKVQBEFEHINGRWMSPLMPDDSADSKKSSRASSFKTSTFTEABAYNSPCT
SKPATPAPSEKGEGIRTPLEKEEAANQEEKPEKNSRIGEKMETEADAPSPAPSLGERL
SKPATPAPSEKGEGIRTPLEKEEAANQEEKPEKNSRIGEKMETEADAPSPAPSLGERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGVKKRKRGPKKQKENKPGKPRKRKKRDSEEEFGSERDEYREKSESGGSEYGTGPGRK
RRRKHREKKEKKTKRRKKGEGDGGQKQVEQKSSATLLLTWGLEDVEHVFSEEDYHTLT
NYKAFSQFMRELTAKKNPKIPMSKMMTILGAKWREFSANNPFKGSAAAVAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVAEQVSAAVSSATPIAPSGPPALPPPPPAADIQPPPIRRAKTKEGKGPGHKRRSKSPR
VPDGRKKLRGKKMAPLKIKLGLLGGKRKKKGGSYVFQSDEGPBPEAEESDLDSGSVHSA
                                EPRKI PLEDEVPGVPGEMEPEPGYRGDREKSATESTPGERGEEKPLDGQEHRERPEGE
TGDLGKREDVKGDRELRPGPRDEPRSNGRREEKTENPRFMFNI ADGGFTELHTLWQNE
ERAAI SSGKLNEI WHRRHDYWLLAGI VLHGYARWQDI QNDAQFAI I NEPFKTEANKGN
                                                                                                                                                                                                                                                                                                                                             FKNMPAKTELI URVELS PMOKKYYKY I LTRNFEALNSRGGGNOVSLLNI MMDLKKCCN
HPYLF PVAAMES PKL PSGAYEGGAL I KSEGKLMILDKMLRKLKEGGHR VL I FSOVTKM
LDLLEDFLDYEGYKYER I DGGI TGALAROEA I DRENAPGAOOTCFLLSTRAGGIG-I INA
TADTVI I FDSDMNPHND I QAFSRAHR I GOANKVMI YR FVTRASVEER I TQVAKRKMML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGRPDGPVRTKKLKRGRPGRKKKKVLGCPAVAGEEEVDGYETDHQDYCEVCQQGGEII
FLEMKNKFLARRFKLLEQALVIEEQLRRAAYLNLSQEPAHPAMALHARFAEAECLAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="zinc-finger helicase"
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/db_xref="GI:3298562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (13-DEC-1996) UPR41, CNRS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="hZFH"
|51. .6153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MKAADTVILWARSKNDQLRISFPPGLCWGDRMPDKDDIRLLPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Snf2-like helicase family"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome="17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
 1406
                                                                                                                                             532 AGGACGAGTGTGCCGTGTGTCGGGAGCGGGGGGGGGGCTCATCTGCTGTGACGGCTGCCCTC 591
                                                                                                                                                                                                         Similarity
                                 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCCGGGCAGAGGA 706
                                                                                          GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                             AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
GCTGCCCTCACTGTGAGAAGGAGGGGGGTCCAGTGGGAGGCCAAGGAGGAAGAAGA 1460
                                                                GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                  3010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="hdzH"
/note="encodes putative zinc-finger helicase formed from
alternative splicing; mRNA observed, but no protein yet
identified; hZFH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(151. .5074,5177. .6153)
                                                                                                                                                                                                                                                                                  /gene="hZFH"
                                                                                                                                                                                                                                                                                                                                                  /note="encodes
3010. .3060
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="encodes
2239. .2259
                                                                                                                                                                                                                                                               'note="polyA_site"
                                                                                                                                                                                                                                                                                                  /note="encodes nuclear targeting sequence"
$744. .6749
                                                                                                                                                                                                                                                                                                                                                                                gene="hZFH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="encodes zinc-finger region"
|525. .1650
                                                                                                                                                                                                                                                                                                                                gene="hZFH"
                                                                                                                                                                                                                                                                                                                                                                                                                 note="encodes"
                                                                                                                                                                                                                                                                                                                                                                                                                              gene="hZFH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="hZFH"
                                                                                                                                                                                                      3.98;
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                                                                                                                                                                                                      Score 59.8; DB Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                               ATPase/helicase domain"
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                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                     72;
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                                                                1405
                                                                                            651
                                                                                                                           1345
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KEYWORDS SOURCE DEFINITION ACCESSION VERSION RESULT 77 AC135674/c REFERENCE Snoor AUTHORS ORGANISM RS Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Baldwin, D., Bandaranaike, D., Barber, M., Byth, P., Brown, M.,
Balakr, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Bhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K.,
Bgan, A., Escotto, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, K.,
Harvey, V., Havis, A., Henderson, N., Hernandez, J., K., LN84/9 bp DNA linear Rattus norvegicus clone CH230-368023, WORKING DRAFT AC135674 Rattus norvegicus (Norway rat) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP Rattus. AC135674.2 GI:25007200 (bases 1 to 168479) Hawes, A., Henderson, N., Hernandez,J. HTG 15-NOV-2002 SEQUENCE.

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Hernndes, R., Mitnes, S., Miladm, S. L., Hodgeon, A., Hoguse, M., Houlins, B., Howelis, S., Mily, K., S., Mily, K., S., Mily, K., S., Mark, J., Johnson, R., Litt, J., Litt,
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REFERENCE AUTHORS TITLE

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SOURCE
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VERSION
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AC119782/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 115;
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                                                                                                                                                                                                                                                                                                     ORGANISM
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 16479: contig of 168479 bp in length.

Location/Qualifiers
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1 (bases 1 to 221787)

Muzny, D.Marie, , Metzker, M.Lee., Abramzon, S., Adams, C., Alc Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benz Baldwin, D., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
                                                                                                                                                                                                                                                                                                AC119782.5 GI:23670853
HTG; HTGS-PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                              Rattus.
                                                                                                                                                                                                                                                Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; |
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                    AC119782
                                                                                                                                                                                                                                                                                                                                                                                                                      AC119782 221787 bp DNA lir
Rattus norvegicus clone CH230-134M24, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCTACCACTTGCACTGCCTCAACCCGCCGCCGCCGGAGATCCCGAACGGTGAATGGCT 12438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGTTCTGCCGCGTGTGCAAGGACGGTGGCGAGCTTCTGTGCTGTGATGCTTGTCCCTC 12498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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/note="clone_boundary
clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end_sequence:BZ145823"
complement(166515...16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="CH230-368023"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _sequence:BZ145824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.9%;
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Pred. No. 0.076;
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                                                                                                   Barnstead, M., Benahmed, F.,
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                                                                                                                                                                             Adams, C., Alder, J.,
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          Chen, Z., Chu, J.,
                                                                                                                                                                                                                                                     Euteleostomi;
; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 12-OCT-2002
SEQUENCE.
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Cleveland.C. . Cockeell.R. Cox.C. Coyle.M. Cree.A. P. Scuzal., Davida M. Li. Davis C. Davy.Corroll Li. De bada C. Devacht.b. Delagado.D. Denson S. Deragor.C. Didg.Y. Ellid.H. Divya.K. B. Deragor.H. Degan-Rocha.S. Damn.A. David.C. David.C. Divya.K. B. Eggn.A. Escotto.M. Supers.C. Resast.C.A. Fall.T. Fan.G. Fernandez.S. Filiay.M. Fall. G. Rass.C.A. Fall.T. Fan.G. M. Forter.M. Ganar. G. S. Filiay.M. Fall. F. Fasas.C.A. Fall.T. Fan.G. M. Farl. F. Farl.
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

(bases 1 to 246566)

REFERENCE

AUTHORS TITLE JOURNAL

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RESULT 79
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                                                         SOURCE
ORGANISM
                                                                                                                                                          ACCESSION
                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                 66660 CCCCGCCCGGCCCGGCCCGGCC 66634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66780 CTCCTACCACTTGCACTGCCTCAACCCGCCGCTGCCGGAGATCCCGGAACGGTGAATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 653 GTGCTCCAGCTGCCTGCAGGCCAACAGTCCAGGAGGTGCAGCCCCGGGCCAGAGGAGCCCCCG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 GGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAG 652
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                            AC097926 246566 bp DN Rattus norvegicus clone CH230-44J16,
                                                                                                                                                       unordered pieces.
AC097926
                                                                                                                                AC097926.6 GI:30521120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h

NOTE: This is a 'working draft' sequence. It currently

consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

provided by the submittor.

This sequence will be replaced

by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCCAGGAGCCACCCGTGGAGACCCC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCCGCGCTGTACAGTGAGTGTTACACCTCCTGCCCCGCCCCGCCCCGCCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGTTCTGCCGCGTGTGCAAGGACGGTGGCGAGCTTCTGTGCTGATGCTTGTCCCTC 66781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACGAGTGTGCCGTGTCGGGGACGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the accession number will be preserved.

1 221787: contig of 221787 bp in length.
Location/Qualifiers
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Center clone name: CH230-134W24

Center clone name: CH230-134W24

Center clone name: CH230-134W24

Center Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 207183 bases at least Q40

Consensus quality: 208452 bases at least Q20

Consensus quality: 208456 bases at least Q20

Estimated insert size: 215799; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="wgs_contig"
complement(220394...2
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end_sequence:BH349190"
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site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'clone="CH230-134M24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59.8; DB 2;
Pred. No. 0.073;
0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .221263)
                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                            WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                              SEQUENCE,
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AUTHORS

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REFERENCE
AUTHORS
TITLE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyael, A., Ayodej, M., Baca, E., Badden, H., Mayael, A., Ayodej, M., Baca, E., Badden, H., Barlen, C., Voyael, A., Ayodej, M., Baca, E., Badden, H., Barlen, C., Chacko, J., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Checko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chere, R., Cortell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, M., Egoct, C., M., Ganta, R., Garcia, M., Garra, M., Garra, M., Gabris, C., M., Falls, T., Fan, G., Chen, E., Chen, C., Chen, C.,
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:23096446.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaze, Houston, TX 77030, USA 3 (bases 1 to 246566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 246566)
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Query Match
Best Local Similarity
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148705 CCCCGCCCGGCCCGGCCCGGCC 148679
                                                                                                                                                                                                                         148825 CTCCTACCACTTGCACTGCCTCAACCCGCCGCCGCCGGAGATCCCGAACGGTGAATGGCT 148766
                                                                                                                                                                                                                                                                                                                                                                                           533 GGACGAGTGTGCCGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft.

* NOTE: This is a 'working draft.

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact size of are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                                               GTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCG 712
                                                                                                                                                                                                                                                                              GGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAG
                                                                                                                                                                                                                                                                                                                                      GGAGTTCTGCCGCGTGTGCAAGGACGGTGGCGAGCTTCTGTGCTGATGCTTGTCCCTC 148826
                                                    GCCCCAGGAGCCACCCGTGGAGACCCC 739
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Center clone name: CH230-44J16

Center clone name: CH230-44J16

Center clone name: CH230-44J16

Center Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 234382 bases at least Q40

Consensus quality: 237163 bases at least Q20

Consensus quality: 239522 bases at least Q20

Estimated insert size: 246580; sum-of-contigs estimation quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end_sequence:BH294325"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_end:Sp6
site:EcoRI
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complement (243583.
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site:EcoRI
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1 244690: gap of unknown length
1 246566: contig of 1876 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2917. .3566
/note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="clone_boundary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%; Score 59.8; DB 2; 55.6%; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence: BH294324"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
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ACCESSION
VERSION
KEYWORDS
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                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
              653 GTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                          Sequence
Ax655393
                                                                                                                                                                         Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. & Plant genes involved in defense against pathogens Patent: WO 03000898-A 5263 03-JAN-2003; Syngenta Participations AG (CH)
                                                                                                                                                                                                                                                           Oryza sativa
Ouranderyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQ720332
Sequence 6266 from Pate:
CQ720332
CQ720332.1 GI:42281189
                                                                                                                                                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 02068579-A 6266 06-SEP-2002; PE Corporation (NY) (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                         /organism="Oryza sativa"
/mol_type="unassigned DNI
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Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishi,J., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Kateuta,M., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
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Homo sapiens cDNA FLJ16830 fis, clone UTERU30
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                         1271
                                                                                                                                                                                                                                                                                  1211 AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGATACCTGTCCCC 1270
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                                                                                                                                                                                                                                                                                                                       532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-701-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (B-mail:genomics@hri.co.jp, Tel:s1-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and
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Isogai,T. and Yamamoto,J.
Direct Submission
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NEDO human cDNA sequencing project
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GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGGAG 1368
                                                              GGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTG 689
                                                                                                                                                                                     GGGCCTTCCACCTGGCCTGCCCTGTCCCGCTCCGGGAGATCCCCCAGTGGGACCTGGA
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="cloning vector: pME18SFL3"
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clone_lib="UTERU3"
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/clone="UTERU3022536"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP better of the property of the subclone and the surface of the surfa
                                                                                                                                                                                                                             593 GGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAG 652
                                                                                                                                                                                                                                                                                                                                                                       533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
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AL611985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 219205)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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/db_xref="taxon:10090"
/chromosome="4"
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/clone_lib="RPCI-23"
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Pred. No. 0.14;
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m clone RP23-421E12 on chromosome 4, complete
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                      exon
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                                                                                                                                                                                                           1209 GAG 1211
                                                                                                                                                                                                                                                            1149 GATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAGTCCCTTCTGAGC 1208
                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                              60;
                                                                                                                                                                                                                                           _
                                                               BC060721 4343 bp mRNA line
Mus musculus chromodomain helicase DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-JUN-1996) Nobuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (B-mail:shimizu@dmb.med.keio.ac.jp, Tel:03-3351-3370, Fax:03-3351-2370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagamine, K., Kudoh, J., Asakawa, S., Abe, I., Maeda, H., Tsujimoto, Minoshima, S., Ito, F. and Shimizu, N. Localization of 22 Exons to a 450-kb Region Involved in the Autoimmune Polyglandular Disease Type I (APECED) on Choromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kudoh, J., Nagamine, K., ABakawa, S., Abe, I., Kawasaki, K., Maeu Tsujimoto, S., Minoshima, S., Ito, F. and Shimizu, N. Localization of 16 exons to a 450-kb region involved in the autoimmune polyglandular disease type I (APECED) on human chromosome 21q22.3
                  BC060721.1 GI:38511411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D86113.1 GI:2244722
HC21EXc33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D86113
Homo sapiens gene for HC21EXc33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimizu, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 4 (1), 45-52 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D86113
                                                  (cDNA clone
                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HC21EXc33"
                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="HC21EXc33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="B-lymphoblastoid"
/clone_lib="chromosome 21-specific cosmid library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ".=qam/
                                                IMAGE: 6406263), partial cds
                                                                                                                                                                                                                                                                                                                             3.8%;
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                                                                                                                                                                                                                                                                                                            Score 58.2; Di
Pred. No. 0.56
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                               Length 63;
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                                                                 protein 3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                   ROD 25-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 04-JUL-1997
                                                                                                                                                                                                                                                                                                            0,
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REMARK
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AUTHORS
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ORGANISM
Ś
                                                                                                                                                                                                      ORIGIN
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                                                                      Query Match
Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
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RS Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 125 Row; f Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Mr. Bento Soares, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg,R.
Direct Submission
Submitsed (03-NOV-2003) National Institutes of Health, Mammalian Submitted (03-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodrique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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   AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 4343)
                                                                                                                                                                                                                                                        /tissue_type="Brain, enri
/clone_lib="NIH_BMAP_FOO"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                clone="IMAGE: 6406263"
                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:10090"
                                                                                                    58.3%;
                                                                         0
                                                                      Score 58.2; DB Pred. No. 0.28; Mismatches
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                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                     mouse brain 12.5dp"
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                                                                         Indels
                                                                                                                                      Length
                                                                                                                                         4343;
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512

AGGATTACTGTGAGGTGTGCCAGCAGGGGGGGAAATTATTCTGTGCGACACCTGCCCCC

571

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REFERENCE
AUTHORS
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                                                                                                                                                                                       AL Submitted (14-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 116984)

Birren, B., Nubbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Hortcon, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Matchews, C., WcCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Marthews, C., WcCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Melnga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanović, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Myman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Liu, G., MacCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Macli, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vas, Milson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Embek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            632
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Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 1, 2003 this sequence version replaced gi:27369450.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mamman, ...
1 (bases 1 to 116984)
1 (bases 1 to 2000)

Birren, B., Nusbaum, C. and Lander, E.

Birren, B., Nusbaum, C. and Lander, E.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,E., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
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AC104581
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Birren,B., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                         Homo sapiens chromosome 17, clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGA 651
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----- Project Information
Center project name: L28162
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                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens chromosome 17, clone RP11-1099M24, complete sequence
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41001: gap of 100 bp
78861: contig of 37860 bp
78961: gap of 100 bp
116984: contig of 38023 bp
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nagos, B., Heaford, A., Horton, L., Kulme, W., Illev, I., Johnson, R., Lamazares, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McMeneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travvis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL Submitted (10-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 187718)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelland, K., Collymore, A., Cook, A., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., MacConald, P., Major, J., Menus, J., Matthews, C., McCarthy, M., MacConald, P., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., Oliver, J., Peterson, K., Seman, S., Severy, P., Senth, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbe, M., Talamas, J., Yeshataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wynan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zodv, M.
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boushawkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Menderim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Norbu, C., O'Connor, T., O'Donnell, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Senty, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Calling, R., Stanger, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Stanger, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                               Submitted (13-MAY-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 13, 2003 this sequence version replaced gi:29150453. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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complement(23383. .23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="<30 qual SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4209. .4468
/rpt_family="MIR"
                                                                                                                                                                                        ) rpt
                                                                                                                                                                                                                                                                   complement (23661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="C-rich"
11178. .11217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="(CCA)n"
10626. .10654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10077. .10135
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clone_lib="RPCI-11 H
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                                                                                                                                                                                                                                                 _family="MIR"
                                                                                                                                                                                                                                                                  family="AluJo"
ement (2267)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         _family="C-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="(CAG)n"
                                                                                                    family="AluSx"
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                                             family="MIR"
                                                                                                                              family="Tigger4 (Zombi)"
                                                                                                                                                                                       family="AluSq"
                                                                                                                                                                                                                     family="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99;
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burreil, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                                                                                                                                                                                                   AC111597 4 GT:24818936
AC111597.4 GT:24818936
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                      AC111597 232984 bp DNA linear HTG 09-NOV-2002
Rattus norvegicus clone CH230-150P11, WORKING DRAFT SEQUENCE, 3
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                               Rattus norvegicus
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                                                                                                                                                                                                                                                                                       unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                            (bases 1 to 232984)
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complement(29321. .
/rpt_family="Aluy"
29776. .30152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="MIR"
compTement(34899..35191)
/rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_fam11y="nature", complement(34143, .34263)
/rpt_family="AluJo"
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complement(33823..338
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32717
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7. .34147
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ement /acr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="AluSx"
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family="L2"
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ement (30860)
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COMMENT

Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/

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Cleveland, C., Cocktell, R., Cox, C., Coyle, M., Cree, A., D'Souazi, L., Davis, C., Davis, C., Coyle, M., Cree, A., D'Souazi, L., Davis, C., Davis, C., Coyle, M., Cree, A., D'Souazi, L., Delyado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregeorgia, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guerra, W., Guartelle, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Handerson, N., Hernandez, J., Hollins, B., Howells, S., Hladm, S. L., Hodgson, A., Hogues, M., Hernandez, J., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kally, S., Kally, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraff, C.L., Labow, H., Lorado, R. J., Levis, L., Liz, Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, M., Malloy, K., Mangum, A., Wangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mayminey, S., McLedd, M. P., Martin, K., Martin, R., Martinez, E., Margum, A., Mangum, S., Mapua, P., Martin, K., Martin, R., Martinez, E., Margum, A., Margum, S., Mangum, A., Margum, S., Mangum, A., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Real, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, L., Pfennkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfennkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfennkoch, C., Sanders, M., Scherer, S., Scott, G., Shatsman, S., Sheen, H., Sheet, M., Storn, R., Ser, R., Ruiz, S. J., Sheet, J., Sheet, S., Stefer, S., Scott, G., Shatsman, S., Sheen, H., Sheet, J., Sheet, S., Sheet, S., Stefer, S., Stefer, S., Stefer, S., Mang, J., Walter, P., 
                                                                                                                                                                                                                                         Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, X77030, USA
On Nov 9, 2002 this sequence version replaced gi:23264551.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-FEB-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 232984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 232984) Worley, K.C.
                                    shotgun sequence table.
                                                                         may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Genome Center
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RESULT 89
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                                                                                                   KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   529 ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCC 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87;
                                                                                                                                                   261384 bp DN Rattus norvegicus clone CH230-164A18, ***, 2 unordered pieces. AC115415
                                                 Rattus norvegicus
                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                                                                                       AC115415
AC115415.3 GI:23266199
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                        Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

(see http://www.nggc.bcm.tmc.edu/docs/cenbank_draft_data.html).

**NOTE: This is a 'working draft' sequence. It currently

**Consists of 3 contigs. The true order of the pieces

**is not known and their order in this sequence record is

**arbitrary. Gaps between the contigs are represented as

**runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                   GGAGGTGCTCCAGCTG 664
                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCTTCCTACCATATCCACTGTCTGAACCCCCCGCTGCCAGAGATCCCAAATGGCGAAT 73108
                                                                                                                                                                                                                                                                                                                                             GGCTCTGTCCCCGCTG 73124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGGGCCTTCCACCTGGCCTGCCTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved
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Center project name: GMQL
Center clone name: CH230-150P11
Center clone name: CH230-150P11
Assembly program: Phrap; version 0.990329
Consensus quality: 199152 bases at least Q40
Consensus quality: 199686 bases at least Q30
Consensus quality: 200691 bases at least Q20
Estimated insert size: 204955; sum-of-contigs estimation
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-150P11"
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                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-MAR-2002) Human Genome Sequencing Center, Departed Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA (bases 1 to 261384)
Rat Genome Sequencing Consortium.
Direct Submission
                                                                                                                                              On Sep 21, 2002 this sequence version replaced gi:21737235. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
                                                                                                                                                                                                                                                                                             Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Worley, K.C.
contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                            sequence may extend beyond the ends of the clone and there may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                          162918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 ATGAGGACGAGTGTGCCGTGTCGGGACGGCGGGGGGGGCTCATCTGCTGTGACGGCTGCC 588
AC123167 278068 bp [Rattus norvegicus clone CH230-70G17, ***, 12 unordered pieces. AC123167 AC123167.4 GI:24635638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                          GGCTCTGTCCCCGCTG 162933
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Center clone name: CH230-164A18
Center clone name: CH230-164A18
Center clone name: CH230-164A18
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 215637 bases at least Q40
Consensus quality: 21565 bases at least Q30
Consensus quality: 21565 bases at least Q20
Consensus quality: 21565 bases at 
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clone_end:T7"
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-164A18"
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 6, 2002 this sequence version replaced gi:23664632.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas
                                                                                                                                                                                                                                                               Submitted (29-MAY-2002) Human Genome of Molecular and Human Genetics, Bayl Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 278068)
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Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  table.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-70G17
Center clone name: CH230-70G17
Center clone name: CH230-70G17
Center clone name: CH230-70G17
Consensus quality: 247200 bases at least Q40
Consensus quality: 251369 bases at least Q30
Consensus quality: 254316 bases at least Q20
Estimated insert size: 246345; sum-of-contigs estimation
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265232
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266774
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267998
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269265
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250760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
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/361. .64450
/note="clone_boundary
clone_end:T7
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/note="clone_boundary
clone_end:T7
                                                         end_sequence:BH274648"
7361. .64450
                                                                                                             site:
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
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91481: gap of unknown length
236448: contig of 144967 bp in length
236548: gap of unknown length
250659: contig of 14111 bp in length
250759: gap of unknown length
260976: contig of 10217 bp in length
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236548:
250659:
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270430: contig of 1166
270530: gap of unknown
278068: contig of 7538
                                                                                                                                                                                                                                                               type="genomic DNA"
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6: contig of 1050 bp in length
6: gap of unknown length
3: contig of 1027 bp in length
3: gap of unknown length
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contig of 1124 bp in l
gap of unknown length
contig of 1067 bp in l
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission

Submitted (09-APR-2004) Wellcome Trust Sanger Institute, Hinxton, Submitteed (19-APR-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries:

zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 5, 2004 this sequence version replaced gi:45433987.
together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
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                                                                                                                                                                                                                                                                                                                                                              Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 189081)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
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clone end:T7"
250760 . 251764
/note="wgs end_extension
clone_end:T7"
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clone_end:T7"
248920. .250659
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91482. .93662
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Pred. No. 0.19;
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526 AGAATGAGGACGAGTGTGCCGTTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCT 585
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Sequence 7389 from Pater
CQ721455
CQ721455.1 GI:42282312
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Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                           Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and oth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson
                                                                                                                                                                                                                                                                  Patent: WO 02068579-A 7389 06-SEP-2002; PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                     Venter, C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-57K11 strom a CHORT-211 BAC library
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llarity 62.9%;
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7389 from Patent WO02068579.
                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                               Location/Qualifiers
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/db_xref="taxon:7955"
/clone="CH211-57K11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Danio rerio"
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                                                                                                                                                                                                                                . 2803
                                                                                                                                                                                                                                                                                                                                                                     Adams, M.C.,
                                                                 Score 56.6; DB Pred. No. 0.62; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56.8; DB Pred. No. 0.29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     Li, P.W. and Myers, E.W
                                                                                                           DB
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                                                                   89;
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                                                                                                         Length 2803;
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AB002296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2105 AGAATGAGGACTTCTGTGCTGTTTGCCTCAATGGCGGAGAGTTACTGTGCTGTGACCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646 CCTGGAGGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 GCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-MAR-1997) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913) On Dec 23, 1999 this sequence version replaced gi:2224536. Sequence updated (20-Dec-1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes VII. The complete sequences of 100 new cDNA clones from brain can code for large proteins in vitro
DNA Res. 4 (2), 141-150 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 6505)
Ohara,O., Nagase,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagase,T., Ishikawa,K., Nakajima,D., Ohira,M., Seki,N.,
Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB002296
AB002296.2 GI:6634008
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Homo sapiens mRNA for KIAA0298 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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/translation="Celiscpgcervyltrdytehfflhcvpteopkmarncseckek raahtlctycnemicsscteerhengeveggfeperaokgspgvunggegdptlycplht obviklfcetycnmltcsscteerhengeveggfeperaokgspgvunggegdptlycplht obviklfcetetendltchscluvehkengerpeperaokgspgvunghengeverkksseg trakcetetengeretengerefergelingerkkeleggerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergerefergere
                                                                                                                                                                                                                                                                                                                                                                                                /note="Start codon is not identified. hf00341 cDNA clone for KIAA0298 has a 1857-bp insertion between 982-983, a 71-bp deletion at the region from 3002 to 3072, and a 290-bp deletion at the region from 3178 to 3467 of the sequence of KIAA0298"
                                                                                                                                                                                                                                          /product="KIAA0298 protein"
/protein_id="BAA20758.2"
/db_xref="GI:6634009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hf003411"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="KIAA0298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="brain"
clone_lib="pBluescriptII
                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="KIAA0298"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                         Submitted (01-DEC-1999) Molecular and Human Genetics/HHMI, Bay
College of Medicine, T634, Mail Stop BCM235, One Baylor Plaza,
Houston, TX 77030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beckstead,R., Ortiz,J.A., Sanchez,C., Prokopenko,S.N., Chambo
Losson,R. and Bellen,H.J.
Bonus, a Drosophila homolog of TIF1 proteins, interacts with
nuclear receptors and can inhibit betaFTZ-F1-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eucaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
AF210315
                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 5811)
Beckstead, R.B., Prok
                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription
Mol. Cell 7 (4), 753-765 (2001)
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LSQTKSPQHLQQTIVGQINY UVQPAPVQSQSQEETLQATDEPBASQGSKEALFLDKN
TAAALPQASGEETPLSVP PVDSTI QHASPAVVRKHSTSLS IMGFSNTLEMELSSTRLE
RPLEPQI GSVSNLTAGAPQAVPSLLSAPPKMVSSLTSVQNQAMPSLTTSHLQTVPSLV
HSTFQSMPNLI SDSPQAMASLASDHPQAGPSLMSGHTQAVPSLATCPLQSI PVSDMQ
PETGSSSSSGFTSGSLCPRDGADPSLENALCKVSPGEMLSKLPLFI I QQXI GHWDPYS
DLSLTVLRPLMTTMSEFFDSCRHPTFERWKVR I PLASLTYWDKVP"
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                                                                 /gene="bon"
694. .4095
                                                                                                                                                                                                     /organism="Drosophila melanogaster"
|mol_type="mdNA"
|db_xref="taxon:7227"
|chromosome="3"
note="TIF1-like protein; BON"
codon_start=1
                                                                                                                                  gene="bon"
                                                                                                                                                                              map="92E8-14"
                                                gene="bon"
                                                                                                               . 693
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                                                                                                                                                              . 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ortiz, J.A., Sanchez, C., Prokopenko, S.N., Chambon, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Prokopenko, S.N. and Bellen, H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56.6; DB Pred. No. 0.54; 0; Mismatches
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                                                                                                                                                                 3499 GAGAGCTGGCAGTGCCTACTGTGCGTCAACATCAAGGAGCTG
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                                                                                                                                                                                                                                                                                                            528 AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGAGCTCATCTGCTGTGACGGCTGC 587
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                                                                                                                                                                                                                                                                                                                                                   96;
 Drosophila
Drosophila
                                             CQ583074 6124 bp DN Sequence 10832 from Patent WO0171042. CQ583074 GI:41644029
                                                                                                                                                                                                                                                                                                                                                                   Similarity
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ALGLGPAVSILSNVTSTIPKTPSPSTHENTKOPTEPIDKVRDDSINDLIATIAKLDSN
GYQVLPEGRTKTTSPQVHSSTDLSNTQEVNNKNEQKDDPNEDWCAVCLDGGELMCCDK
CPKVPHQNCHIPAISSLPDESBSWQCLLCVNIKELTKTEGSEKSSGELSALELERICDK
RICLELYCQYEGSLNFRSPESPANTSYYEIVSSPMSLDVIRTRLDPSSPNHYKDIAGF
VSDVRLIFSNTYLFYQEDTKTYSNAKYLENFFEEQLAKWLPQFEGTKPQGKRNTSNSP
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/gene="bon"
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3571. .3909
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/protein_id="AAF19646.1"
/db_xref="GI:6631000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="bon"
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Pred. No. 0.6;
0; Mismatches
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Matches 96
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Best Local Similarity
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                                                                                                                                                                                                          96;
                                                                                                                                                                                                                                                                                                                                                                         Venter, J.C., Adams, M., Li, P.W. and Myers, E.W. Detection kits, such as nucleic acid arrays, for expression of 10,000 or more Drosophila genes and Patent: WO 0171042-A 10831 27-SEP-2001; PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila sp.
Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10831 from Pat
CQ583073
CQ583073.1 GI:41644028
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Detection kits, such as nucleic acid arrays, for detecting the
expression of 10,000 or more Drosophila genes and uses thereof
Patent: WO 0171042-A 10832 27-SEP-2001;
PE Corporation (NY) (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQ583073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drosophilidae; Drosophila
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GAGAGCTGGCAGTGCCTACTGTGCGTCAACATCAAGGAGCTG 17971
                                                                                       CCTCGGGCCTTCCACCTGGCCTGCCTGCCTCCGCTCCGGGAGATCCCCAGTGGGACC
                                                                                                                                    AACGAGGACTGGTGCGCCGTCTGTCTGGATGGAGGCGAGCTGATGTGCTGCGACAAGTGT 17865
                                                                                                                                                      AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC 587
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                                TEGAGETECTCCAGCTECCTECAGECAACAGTCCAGGAGGTE
                                                                  CCCAAAGTTTTCCATCAGAACTGTCACATCCCTGCGATCAGCTCGTTGCCGGACGAGAGC
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                                                                                                                                                                                                                                                                                     /organism="Drosophila
/mol_type="unassigned
/db_xref="taxon:7242"
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/mol_type="unassigned
/db_xref="taxon:7242"
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .21747
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                                                                                                                                                                                                      Score 56.4; DI
Pred. No. 0.49
0; Mismatches
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Pred. No. 0.6;
0; Mismatches
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d uses thereof
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TITLE
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AC017943
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Best Local S
Matches 96
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ISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hrsapoda; Insecta; Pterygota;

Eukaryota; Metazoa; Arthropoda; Hrsapoda; Insecta; Pterygota;

Roptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

CE 1 (bases 1 to 170339)

CE 1 (bases 1 to 170339)

RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

Carison, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dreenek, D., Farfan, D.,

Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,

Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,

McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9493
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AC017943
AC0179431 GI:6553247
HTG; HTGS_PHASE2.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 97538)
1 Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10212734 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                 AC007757.5
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the accession number will be preserved.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Pred. No. 0.38
0; Mismatches
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AC007771
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Best Local Similarity
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             Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 197071)

***Common Profession P
                                                                                                                                                                                                                                                                                                  HTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (07-JUN-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 15, 2001 this sequence version replaced gi:6598748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler, Stapleton,M., Strong,R., Svirskas,T., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. Sequencing of Drosophila chromosome 3R, region 928-92F
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    Celniker, S.E.,
                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                     AC007771.7 GI:12831351
                                                                                                                                                                                                                                                                                                                                                                                                           BACR26M03, complete
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/clone lib="RPCI-98 (Roswell Park Car
Drosophila melanogaster BAC library,
pBACe3.6)"
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/db_xref="taxon:7227"
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|mol_type="genomic DNA"
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Adams, M.D., Kronmiller, B.,
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library, partial EcoRI in
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Tyler, D., Wan, K.H.,
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[B. 20]
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location For further information about this sequence visit our sequence

For further information about this sequence, please visit our sequence

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Drosophila melanogaster chromosome complete sequence. AE003731 AE002708 AE014297
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2 (clinker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Celniker, S.E., Agbayani, A., Chavez, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Karra, K., Kearney, L., Kim, B., Levis, S., Li, P., Lomotan, M., Mazda, P., Kim, B., Levis, S., Li, P., Lomotan, M., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Prishas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Britishas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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Drosophila melanogaster BAC library, partial EcoRI
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/mol_type="genomic_DNA"
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RRS Adams, M.D., Celniker, S.E., Holt, R.A., Wanns, C.A., Gocayne, J.D., Amanatidee, P.G., Scherer, S.E., Li, P.W., Hookine, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Aehburner, M., Henderson, S.N., Stuton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Hardon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Baxendale, J., Bayaktaroglu, L., Beasley, E.M., Barkow, P. V., Berman, B.P., Bandari, D., Botshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Broktein, P., Brottier, P., Canders, R., Bouck, J., Broktein, P., Brottier, P., Davies, P., Odeson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Durkov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferr
                                                                                                                        Misra, S., Crosby, M.A., Mungall, C.J., Matthews, B.B., Campbell, K.S., Hradecky, P., Huang, Y., Kaminker, J.S., Millburn, G.H., Prochnik, S.E., Smith, C.D., Tupy, J.L., Whitfied, E.J., Bayraktaroglu, L., Bertencourt, B.R., Celniker, S.E., de Grey, A.D., Drysdale, R.A., Harris, N.L., Richter, J., Russo, S., Schroeder, A.J., Shu, S.O., Stapleton, M., Yamada, C., Ashburner, M., Gelbart, W.M.,
                                                                                                                                                                                                                                                                                                                                                                                       Gibbs, R.A. and Rubin, G.M.
Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence Genome Biol. 3 (12), RESEARCH0079 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 230001)

Celniker, S.E., Wheeler, D.A., Kronmiller, B., Carlson, J.W.,
Halpern, A., Patel, S., Adams, M., Champe, M., Dugan, S.P., Frise, E.,
Hodgson, A., George, R.A., Hoskins, R.A., Laverty, T., Muzny, D.M.,
Nelson, C.R., Pacleb, J.M., Park, S., Ffeiffer, B.D., Richards, S.,
Sodergren, E.J., Svirskas, R., Tabor, P.E., Wan, K., Stapleton, M.,
Sutton, G.G., Venter, C., Weinstock, G., Scherer, S.E., Myers, E.W.,
         Annotation of the Drosophila melanogaster euchromatic genome: a systematic review Genome Biol. 3 (12), RESEARCH0083 (2002)
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The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective Genome Biol. 3 (12), RESEARCH0084 (2002)
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Submitted (06-SEP-2002) University of California
Sciences Addition, Berkeley, CA 94720, USA
7 (bases 1 to 230001)
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Submitted (21-MAR-2000)
Rockville, MD 20850, USA
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ms, M.D., Celniker, S.E.,
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complement (join(11918 . .12780,13429.
15635 . .15835,15894 . .16151,16210. .1
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/locus_tag="CG4257"
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15635. .15835,15894. .16151,16210. .16689,16758. .17788,
17915. .18327,28316. .28547))
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/locus_tag="CG4257"
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| gene="Stat92B"
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/db_xref="GI:28381377"
/db_xref="FUYBASE.FBgn0053192"
/trānslation="MGCKACGTNCQCSATKCGDNCACSQQCQCSC"
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standard; DNA; 1545 BP.  ';  '999 (first entry)  coding a human autoimmune ne regulator-2; AIR-2; in autoimmune polyendocrino autoimmune polyglandular  iens.  Location/Qualifie 237. 1283 /*tag= a /product= "AIR-2;  9-A1.  999.  99-A1.  999; 98WO-FI000749.  999; 97FI-00003762.  FINNISH IMMUNOTECHNOLOGY Heino M, Peterson P, N, Kudoh J;  9-244390/20.	1469 1469 1469 1469 1469 1469 147001 2337 31465 44523 44523 44523 44523 44523 145000 110000 110000 110000 110010
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ALIGNMENTS  1 7 X26937; -JUN-1999 (first entry)  NA encoding a human autoimmune regulator-2 (AIR-2) protein. toimmune regulator-2; AIR-2; immune maturation; immune respondance; autoimmune polyendocrinopathy candidiasis ectodermal ECED; autoimmune polyglandular syndrome type I; APS I; ss. mo sapiens.  Location/Qualifiers y 2371283 /*tag= a /product= "AIR-2" 9915559-A1APR-1999SEP-1998; 98WO-FI000749SEP-1997; 97FI-00003762. TIM-) FINNISH IMMUNOTECHNOLOGY LTD. ohn K, Heino M, Peterson P, Scott H, Antonarakis S, Lalimizu N, Kudoh J; T; 1999-244390/20.	AAQ40323 AAD160528 AAD143517 ACA40697 ADC24019 ADE60227 ADE60227 ADE60229 ADE60233 ADD45822 ADQ240497 ABL30496 AAL199682 29 AAL199682 29 AAC5436 AAL199682 29 AAC5436 AAL19683 39 AAC5436 AAC54
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tt H, Antonarakis S, Lalioti M;
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standard; DNA; 1463 ВP

(first entry)

human autoimmune regulator-3 (AIR-3) protein

Autoimmune regulator-3; AIR-3; immune maturation; immune response; disease; autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular syndrome type I; APS I; ss.

Location/Qualifiers 237. .1001 /\*tag= a /product= "AIR-3"

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Pred. No. 1.1e-208;
0; Mismatches 4;
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GGTGCGCGTTGCGGGGTGTTGCGGAGATGGTACGGACGTGCTGCGGTTGTACTCACTGCGCC
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AAATTAGCTG
                                        AAATTAGCTG
                                                                                       TTCTCTACTCTGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAATATAA
                                                                                                                                 TTCTCTACTCTGGAAGTCCCCGGGAGCCTCTCCTTGCCTGGTGACCTACTAAAAATATAA
                                                                                                                                                                            CAGCTCTGTGTTTTCTGGGGACACCAGCCATCATGTGCCTGGAAATTAAACCCTGCCCCAC
                                                                                                                                                                                                        CAGCTCTGTGTTTCTGGGGACACCAGCCATCATGTGCCTGGAAATTAAAACCCTGCCCCAC
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AAX58605 standard; CDNA; 2245 ВP

(first entry)

Human autoimmune polyglandular disease type 1 (APGD1) cDNA

Autoimmune polyendocrinopathy candidiasis ectodermal dystrophy; APECED; autoimmune polyglandular disease type 1; APGD1; AIRE; human; transcription factor; autoimmune disease; diagnosis; gene therapy; ss.

variation /product= "human\_APGD1"
replace(358,T)
/\*tag= k replace(374,G) /\*tag= 1 replace (708, T) Location/Qualifiers

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02-OCT-1997;
08-OCT-1997;
12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
P-PSDB; AAY06073
                    Peltonen L, Aalton
Horelli-Kuitunen N,
                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                     variation
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                                                                                                                                                    polyA_signal
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                                            (PLAC ) MAX
(NAPU-) NAT
                                                                                                                             WO9918197-A2
                                            PLANCK GES FOERDERUNG WISSENSCHAFTEN PUBLIC HEALTH INST.
                             Aaltonen J,
                                                                 97EP-00117154.
97EP-00117398.
97EP-00119810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= o
/note= "silent polymorphism"
replace(801,T)
/*tag= p
/note= "silent polymorphism"
replace(889,T)
                                                                                                                                        ,note= "Alu sequence overlapping with PFKL promoter
starts at this position"
2191. .2195
/*tag= t
                                                                                                98WO-EP006294
                                                                                                                                                                                                                                                                                                        replace(1284,A)
/*tag= d
/note= "1-nucleotide insertion, results in frameshift
truncated 422 aa protein"
1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= j
/note= "alters Arg codon to STOP, and truncated 256 aa
protein"
                                                                                                                                                                                                                                                    /note= "1-nucleotide deletion, results in frameshift and
truncated 478 aa protein"
replace(1317,T)
                                                                                                                                                                                                              /*tag= e
/note= "l-nucleotide insertion"
                                                                                                                                                                                                                              /*tag= q
/note= "silent polymorphism"
replace(1365,C)
                                                                                                                                                                                                                                                                                                                                                    truncated prote replace (1094, A)
                                                                                                                                                                                                                                                                                                                                                                    /note= "4-nucleotide insertion,
                                                                                                                                                                                                                                                                                                                                                                                  /note= "4-nucleotide insertion,
truncated 371 aa protein"
replace(1090,CCTG)
                                                                                                                                                                                                                                                                                                                                                                                                                        truncated 372 aa protein"
                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= f
/note= "13-nucleotide deletion, results in frameshift
                                                                                                                                                                                                        replace (1698, T)
                                                                                                                                                                                                                                                                                          note= "1-nucleotide deletion"
                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                 replace (1085, CCTG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace (1052, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= g
/note= "l-nucleotide
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                     Yaspo
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                    Bjoerses P,
po M, Lehrach
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                    rses P, Perheentupa J,
Lehrach H;
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                                                                                                                                                                                                                                                                                                                       XFX WXDDDDDDDDDDDDDDDDDDDDDDXX
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Claim 1; Fig 2A; 77pp; English New polypeptide which co-segregates ä mutated

CC This is the nucleotide sequence of human autoimmune polyglandular disease CC type 1 (APGD1 or AIRE) CDNA. It is a composite of 2 clones, which were CC obtained from a human adult thymus CDNA library by PCR (see AAV5609-10), CCC and of a 3'UTR extension PCR product. The encoded protein (see AAV56073) CC is a transcription factor or transcription- associated factor that may associate with vimentin fibres, perhaps as part of a docking mechanism CC prevent formation of vimentin intermediate filaments. Mutated APGD1 CC polypeptides co-segregate with autoimmune polyendocrinopathy candidiasis CC ecidermal dystrophy (APECED). The invention provides vectors and host CC cells for preparation of APGD1 polypeptides. APECED-associated mutations CC found in the APGD1 gene include: an insertion of 4 nucleotides (CCTG), normally found at position 1086-1089, at nucleotides (CCTG), an insertion of an adenosine at position of nucleotides 1095-1097; a cytosine at position 1369; a deletion of nucleotides 1095-1097; a cytosine at position 1309 or 1313; a cytosine to thymidine exchange at position 358; an adenosine to thymidine exchange at position 358; an adenosine exchange at position 1052; and a cytosine to adenosine to adenosine exchange at position 1052; and a cytosine to adenosine exchange to position 1094. A CC position 1052; and a cytosine to adenosine exchange to position 1094. A CC position 1052; and a cytosine to adenosine exchange to position 1094. A CC position to thymidine exchange to position 1094. A CC position 1052; and a cytosine to adenosine exchange to position 1094. A CC position 4 polypeptide. APGD1 nucleic acid can be used in gene CC position 4 polypeptide. APGD1 nucleic acid can be used in gene therapy

Sequence 2245 BP; 419 A; 765 C; 697 Ģ; 364 T; 0 U; 0 Other;

S	CGCTGCAGATCCTCCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCCC 1115	1056 C	Ş
0	GCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTG 1530	1471 G	DЬ
σ.	GCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTG 1055	996 G	ξŠ
0	GGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCC 1470	1411 G	뮍
	GGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTGCTGCTGCGGTGTACTCACTGCGCC 995	936 G	8
٥	TCCTCGGCCCTGCACCCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCT 1410	1351 T	ДЬ
	TCCTCGGCCCTGCACCCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCT 935	876 T	γQ
0	ACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGGCTGGAC 1350	1291 Å	Ъ
	ACTCTTGTCTACAAGCACCTGCCGGCTCCGCCCTTCTGCAGCCCCGCTGCCAGGTCTGGAC 875	816 A	Ş
0	AGGTCGGCGGGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCCGGCATGGACACG 1290	1231 Å	ДЬ
	AGGTCGGCGGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACG 815	756 A	γQ
0	CGGGCAGAGGAGCCCCGGGCCCCAGGAGCCACCCGTGGAGACCCCGCTCCCCCCGGGGGCTT 1230	1171 0	DЬ
	CGGGCAGAGGAGCCCCGGGCCCCAGGAGCCCACCCGTGGAGACCCCCGCTCCCCCCGGGGCTT 755	696 C	ş
0	CCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCC 1170	1111 0	DЬ
	CCCAGTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCC 695	636 C	Ş
0	TGTGACGGCTGCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCTCCGGGAGATC 1110	1051 1	Д
	TGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCCTCCCCTCCGGGAGATC 635	576 T	γŞ
•	CTCCACCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGGGG	991 d	망
	CTGTGCCAGAAGAATGAGGACGAGTGTGCCCGTGTGTCGGGACGGCGGGGAGCTCATCTGC 575	516 C	γQ
•	66.3%; Score 1023.6; DB 2; Length 2245; ilarity 99.6%; Pred. No. 1.1e-208; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Query Match Best Local Similarity Matches 1026; Conser	7 M O

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RESULT 5
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XX AAX5
XX AAX5
XX AULO
DE MOUS
XX AULO
XX A
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12-NOV-1997;
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Best Local Similarity
Matches 580; Conserv
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Claim:6; Fig 14A-C; 77pp; English.
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This is the nucleotide sequence of murine AIRE cDNA. Murine AIRE is the homologue of the human AIRE (or autoimmune polyglandular disease type 1, APGDI) gene (see AAX58605). The overall nucleotide sequence identity between the mouse AIRE coding sequence and that of the human is 76.67%. The mAIRE gene was localised to chromosome 10. Human mutated APGDI cosegregates with autoimmune polyendocrinopathy candidiasis ectodermal dystrophy (APECED). The murine homologue may be used to develop an animal model for APECED, to examine the events that lead to the development of APECED and possibly to develop agents for preventing and/or treating this autoimmune disease

Sequence 1656 BP; 344 A; 532 C; 479 G; 301 T; 0 U; 0 Other;

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Length 1656;

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                                                                                                                                                                                                                                                                                                                                                                                                         macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                 Score 118.4; DB 6
Pred. No. 1.6e-15;
0; Mismatches 46
                                                                                                                  AGGTTTTTAAGAGTATGGCGTTTGGTTTAGGTTGTATTCG
                                                                                                                                                                                                                                                                                                                                                       C; 2928 G; 4727 T;
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                                                                                                                                                                                                                                                                                                                                                       0 U; 0 Other;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                         Length 9876;
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CTACTCTCAACTAAACCCCGTAAATAAACCGAACGCCCCTACTATAACCAAAAAATCAAAA

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RESULT 7
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                                                                                            Matches
                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              diagnosis and treatment methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabettic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                   including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                      Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL32093
                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; antianaemic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-)
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                                       491
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           61
                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS AG
CTGCTCTCAGCTGGGCCGGTGGGTGGGCCCCGGCTATAGCCAGGAGGTCAAGG
                                                                                                                                                9876
                                       AAAAAAATAAAATCTTCTCAAACTCTTAAAAACATAACGTTTAATCCAAACTATACCCG
                                                         AGAGAAAGTGAGGTCTTCAGGCTCTTAAGAGCATGGCGTTTGGTCCCAGGCTGTACCCG
                                                                                                                                                                                                                                                                                                SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGTGTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGGTCGGGAG
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                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000DE-01032529.
2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                               B₽;
                                                                                                                                                                          present sequence is a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system disease; cytosine methylation; antiasthmatic;
                                                                                                                                               1882 A; 309 C;
                                                                                                                                                                                                                                                                                                66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                        6.6%;
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                                                                                                                                                                                                                                                                                                                                      fragment of of diseases
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                                                                                                                                                                                                                                                                                                                                                                                                        Berlin
                                                                                           0,
                                                                                                        Score 101.8; DB 6; Pred. No. 5.6e-12;
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      ~
                                                                                                                                               3154 G;
                                                                                                                                                                                                                                                                                                                                      chemically modified gene, associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:
                                                                                                                                               4531 T; 0 U; 0 Other;
                                                                                                                                                                          of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nootropic;
                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                German.
                                                                                            Indels
                                                                                                                    Length 9876;
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                                                                                           Gaps
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The invention relates to human chromodomain, helicase, DNA-binding 5 CC (CHD5; ADH12180) and cDNA encoding it (ADH12179). CHD5 is a novel member of the CHD gene family, members of which have a profound effect on cof the CHD gene family, members of which have a profound effect on the choice in cell cycle control, regulation of development, and conceptness (CHD5 comprises two N-terminal zinc finger domains of the PHD CC (plant homeodomain) class, two chromodomains, a central region which CC contains a predicted DEAH-box-type helicase domain and a putative SNF2 CC domain, and several nuclear localisation signals. The gene encoding CHD5 is located on chromosome 1p36.3, a region frequently deleted in a variety of cancers including neuroblastoma, and the protein is preferentially CC expressed in brain. CHD5 is therefore thought to be a modulator of normal neural development and neoplasias of neural tissue origin. The invention CC also relates to vectors and host cells comprising the CHD5 cDNA sequence, an antibody against CHD5, a method of screening for modulators of CHD5 activity; a method of diagnosing cancer in a patient, where a reduced CC level or absence of CHD5 or CHD5 nucleic acids indicates the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromodomain helicase DNA-binding 5; CHD5; chromosome 1p36.3; chromatin structure; chromatin unwinding; DNA repair; DNA recombination; transacriptional regulation; gene expression; cell cycle control; development regulation; oncogenesis; brain; neural development; neural tissue neoplasia; diagnosis; cancer; neural cancer; neuroblastoma; breast cancer; colon cancer; liver tumour; germ cell tumour;
                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                    Novel chromodomain helicase DNA-binding (CHD) proteins, useful as diagnostic and prognostic indicator of tumor, comprises amino terminus having two PHD class zinc finger domains and two chromodomains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brodeur GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening; cytostatic; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2004-082186/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHILDRENS HOSPITAL PHILADELPHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH12180.
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCACTAAAAATACCATACTCATCTTTCGTCCCCAACATAATTTCTTAATAAAATAAA 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (chromodomain, helicase, DNA-binding 5)-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002US-0388848P
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RESULT 9
ABN38615
ID ABN3
XX ABN3
AC A
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Best Local
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                                                                                                                                                                                                                                                                                                                            New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000; 2000US-0221607P
02-MAY-2001; 2001US-0287724P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-2001; 2001WO-IB001903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splice variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mouse; rat; splice transcript; detection; RNA transcript;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN38615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulation. The present sequence represents cDNA encoding human CHD5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COMP-) COMPUGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wasserman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcriptome; oligonucleotide library;
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Pred. No. 0.0004;
0; Mismatches 6
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridisting selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The

Example 1; SEQ ID NO 11363; 47pp; English

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                                The invention relates to an isolated polynucleotide comprising a sequence selected from 183 human DNA sequences (appearing as ABK70130-ABK70312), or their fragments, homologues, variants or complements and their encoded polypeptides. Also included are an expression vector comprising the polynucleotide operably linked to an expression control sequence; a host cell transformed or transfected with an expression vector of; an isolated antibody, or its antigen-binding fragment that specifically binds to the polypeptide; a method for detecting the presence of a cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tumor lung proteins and nucleic acids encoding the proteins, useful as vaccines and for treating, preventing, diagnosing or monitoring lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-2000; 2000US-0234837P
10-OCT-2000; 2000US-0239440P
29-JUN-2001; 2001US-0301928P
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    and pathology-specific genes such as those genes only expressed
specific tissue under a specific pathological condition; to detect

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-SEP-2001; 2001WO-US042232
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fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                    Page 146-148; 189pp; English
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    comprising at least the polypeptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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iagnosis; ss.
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Best Local
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05-JUN-2000;
18-SEP-2000;
18-SEP-2000;
20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen, designated Mi-2. The sequence numbering given in the specification starts at nucleotide 91, i.e. the 5' UTR is omitted, as well as the 'A' of the first ATG start codon. The protein is hydrophilic, acidic and protruding regions of the protein are characteristic of helicases. The gene corresponding to this CDNA was localised to chromosome 12 (12p13). The DNA can be used for the recombinant production of Mi-2 which is used for, e.g. the differential diagnosis of collagen diseases, esp. dermatomyositis, e.g. by immunoassay or Western blotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stomach cancer
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Pred. No.
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Weaver Z
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ä Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change expression of a gene of a signature gene

Claim 1; SEQ ID NO 2747; 44pp; English.

The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
cexpression of at least one gene (I) of a signature gene set, where (I)
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
to ABL70110), or is at least 95% identical to (S), where a change in
expression is indicative of anti-neoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. M1 can be used for screening an
anti-neoplastic agent, and can be used for product which is
the data collected with respect to the anti-neoplastic aproduct which is
the data collected with respect to the anti-neoplastic agent as a result
of M1, and the data is sufficient to convey the chemical structure and/or
properties of the agent. M1 can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

Sequence 6417 BP; 1774 A; 1494 C; 1784 G; 1365 T; 0 U; 0 Other;

Query Match Best Local S Matches 96 96; Similarity Conservative 3.9%; 0,: Score Pred. Mismatches NO ; 0.0044; B ٠. ص 60; Length Indels 6417; 0, Gaps

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RESULT 13
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                     chondroblastic phenotype, or hybridising under stringent conditions to them (or their fragments). Also included are expression vectors, transformed host cells, expressed polypeptides or peptide fragments (which induce differentiation of a mesenchymal cell and may be used as an immunogen ), binding partners of the polypeptides, a method for identifying an agent useful in modulating mesenchymal cell and important cell and important cell and induction activity of a molecule, a method of diagnosing a condition characterized by aberrant expression of a nucleic acid molecule or its expression product; a method for determining regression, progression or onset of cartilaginous tissue degeneration condition in a subject characterised by aberrant expression of a nucleic acid molecule or its expression product; a method for treating a cartilaginous tissue degeneration condition, a method for treating a cartilaginous tissue degeneration developing in the risk of cartilaginous tissue degeneration condition, and a solid-phase nucleic acid molecule array consisting essentially of a set of nucleic acid muleicacid acid molecule array consisting essentially of a set of nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to new isolated nucleic acid molecule compris-
nucleic acid molecule consisting of a gene differentially expressed
cells undergoing differentiation from mesenchymal cell to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chondroblastic phenotype; mesenchymal cell; cartilage formation; bone formation; arthritis; osteoarthritis; rheumatoid arthritis; gout arthritis; adjuvant arthritis; arthritis deformans; antigout; infectious arthritis; osteochondrossis; RDA; antiarthritic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules capable of promoting chondrogenesis, useful for diagnosing and treating cartilaginous tissue degeneration conditio e.g. osteoarthritis, rheumatoid arthritis, gout arthritis, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX04169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adult respiratory distress syndrome, inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    technique of representational difference analysis, RDA), its expressiproducts or fragments, fixed to a solid substrate. The nucleic acids, polypeptides and agents are useful for treating cartilaginous tissue degeneration conditions such as osteoarthritis, rheumatoid arthritis, gout arthritis, adjuvant arthritis, arthritis deformans, infectious arthritis, or osterochondrosis. The present sequence is a CDNA from a known gene differentially expressed in developing mesenchymal cells
                                                                                                                                                                                                       Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA differentially expressed in granulocytic cells #1267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6417 BP; 1774 A; 1494 C; 1784
                                                                                                                                                                                                                                                                                                                                                                                       Beazer-Barclay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2000; 2000US-0237189P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiac reperfusion injury; renal reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK84696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK84696 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentially expressed in developing mesenchymal cells using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the

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expression

expression

unactivated

Claim

SEQ

ID NO

1267; 114pp; English

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RESULT 15
AAD54631
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Matches
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                                                                                                                                                                                                                                                       Human; p53 pathway; therapeutic; angiogenic disorder; apoptotic disorder; chromodomain helicase DNA binding protein; CHD; cancer; gene therapy; cell proliferative disorder; chromatin organisation modifier domain;
                                                                                                                                                                                                                                                                                                                                                                            Human chromodomain helicase DNA binding protein (CHD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD54631 standard; DNA; 6417
                                                                                                                                                                                                                                  cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2003
                                                       12-DEC-2002
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                                                                                                                                                                     Homo sapiens
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Pred. No. 0.004
0; Mismatches
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03-JUN-2002; 2002WO-US017466.

12-DEC-2002

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RESULT 16
AAD54632
ID AAD54
XX AAD54
XX AAD54
XX AAD54
XX AAD54
XX Human
XX Human
XX Human
XX Cell
XX Cclue
XX Colon
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10-OCT-2001;
22-OCT-2001;
15-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for identifying candidate p53 pathway modulating agents. The method involves contacting an assay system comprising purified chromatin organisation modifier (chromo) domain helicase DNA binding proteins (CHD), nucleic acids, their functionally active fragments or derivatives, with a test agent under conditions where, but for the presence of the test agent, the system provides a reference activity. The methods are useful for identifying modulators of the p53 pathway as therapeutic targets for disorders associated with defective p53 function, such as angiogenic disorders, apoptotic disorders or cell proliferative disorders, e.g. cancer. The modulators are useful as research reagents, diagnostics and therapeutics. The invention is also useful in gene therapy. The present sequence is human CHD DNA
                                                                                            Human; p53 pathway; therapeutic; angiogenic disc
chromodomain helicase DNA binding protein; CHD;
cell proliferative disorder; chromatin organisat
cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a candidate p53 pathway-modulating targets for disorders related to defective p53 contacting an assay system having purified CHD acid, with a test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Friedman L,
Lioubin MN;
                                                                                                                                                                                                                                                                        AAD54632 standard;
                               WO200298899-A2
                                                                                                                                                                          Human chromodomain helicase
                                                                                                                                                                                                          26-JUN-2003
                                                                                                                                                                                                                                          AAD54632;
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                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                       1318
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                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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2001US-0328605P.
2001US-0338733P.
2002US-0357253P.
2002US-0357600P.
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                                                                                                                                                                                                                                                                        DNA;
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                                                                                                                                                                         DNA binding protein
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Pred. No.
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                                                                                                           genic disorder; apoptotic disorder;
ein; CHD; cancer; gene therapy;
organisation modifier domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 6417;
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                                                                                                                                                                            (CHD)
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RESULT 17
ADP10531
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ADP10
XX
AC ADP10
DT 12-AU
DX
XX
Crans
KW trans
KW infla
XX
CS Homo
OS Homo
OX
PN WO200
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PD 21-M2
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10-OCT-2001;
22-OCT-2001;
15-FEB-2002;
15-FEB-2002;
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                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                           WO2004042346-A2
                                                                            transplant rejection; immune inflammatory bowel disease;
                                                                                                                  Reference
                                                                                                                                                                                                ADP10531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a candidate p53 pathway-modulating targets for disorders related to defective p53 contacting an assay system having purified CHD
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                                                                                                                                                                                                 standard;
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                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy. The present sequence is human CHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2001US-0296076P.
; 2001US-0328605P.
; 2001US-0338733P.
; 2002US-0357253P.
; 2002US-0357600P.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                  sequences
                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 3.9%;
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                                                                            immune system;
sease; multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60;
Pred. No.
                                                                                                                  marker probe
                                                                                                                                                                                                 ВP
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                                                                             rheumatoid arthritis;
sclerosis; HIV; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Francis-Lang
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RESULT 18
AA158444
ID AA158
XX AA158
XX AA58
XX AA58
XX 22-OC
XX Human
XX Human
XX Human
XX Alzhe
KW Alzhe
KW Chemc
KW Chemc
KW Chemc
XX Homo
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Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, are xenotransplant rejection or mechanical organ replacement rejection, in a individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosi and monitoring of allograft rejection and other disorders.
                                                              peripheral nervous system; neuropathy; central nervous system; Calzheimer's; Parkinson's disease; Huntington's disease; haemosta amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy;
peripheral nervous system; neuropathy; central nervous system;
                                                                                                                                                                                                                                                                           AAI58444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                      Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to diagnosing
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                                                   eukaemia; ss.
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nilarity 61.5%;
Conservative
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                                                                                                                                                                                                        (first entry)
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2002US-00325899.
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                                                                      arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or monitoring transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60;
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RESULT 19
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Matches
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19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, canencactic/chemokinetic activity, haemostatic and thrombolytic activity, canecr disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form that the continual c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
Wang
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6475 BP; 1760 A; 1528 C; 1822 G; 1365 T; 0 U; 0 Other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 647; 10078pp; English.
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                23-SEP-2004
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25-APR-2000; 2000US-00552317.
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                                                                                                                                                                                                                                                                                                          532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Wang Z,
Goodrich
                                                                                                                                                                                                                                                      | | GGGCCTTCCACCTGGCCTGCCCTGCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
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                                                                                                                                                                                                                                                                                       AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                              standard;
                                                                                                                                                            GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1482
                                                                                                                                                                                          GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
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ilarity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               printed specification
                (first entry)
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Wehrman T,
h R, Drmanac
                                                                            CDNA; 6475 BP
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, Xu C,
ac RT;
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Xue
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                     Indels
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, Zhao QA;
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Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6475 BP; 1760 A; 1528 C; 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes. The antibodies are useful for detecting or quantitating the polypeptide in tissue. The polypeptides can also be used as molecular weight markers and as a food supplement. This sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New G-protein-coupled receptor-like polypeptides and polynucleotides, useful for treating diseases of ophthalmic, neurological, immunological and nephritic systems and hormonal dysfunction, cancer, atherosclerosis
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neurological disorder; immunological disorder; nephritic disorder;
hormonal dysfunction; cancer; atherosclerosis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
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ilarity 61.5%;
Conservative
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Pred. No. 0.0044;
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Novel human cDNA SEQ ID NO

325.

04-DEC-2003

(first entry)

ADB48415 standard;

CDNA;

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RESULT 21
AAI60230
ID AAI60
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AC AAI60
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Humar
KW Humar
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Best Local Similarity
Matches 96; Conserv
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a polynucleotide comprising a sequence given in the specification, or its mature protein-coding portion, or its complement. The polynucleotide is useful for treating diseases e.g., cancer or neurodegenerative diseases and many others listed in the specification. The present sequence represents a novel human cDNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030104529.
                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide, userur
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25-APR-2000; 2000US-00552317.
19-JUL-2000; 2000US-00620312.
                                                                                                       22-OCT-2001
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TANG Y T.
LIU C.
ASUNDI V.
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Pred. No. 0.004
0; Mismatches
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RESULT 22 ADQ22446 ID ADQ224 XX

ADQ22446

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                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheiner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and course states and the state of the sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2000;
25-APR-2000;
20-JUN-2000;
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                       part
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Wang
Zhou
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03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and
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Wang Z, Wehrman T,
Goodrich R, Drmana
                                                                                                                 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTTGACGGCTGCCCTC
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                 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
                                                GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG
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nilarity 61.5%;
Conservative
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2000US-00653450.
2000US-00662191.
2000US-00693036.
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2000US-00552317
2000US-00598042
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system injuries.
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RESULT 23
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 25-MAR-2003
27-JUL-1992
                                   AAQ22728;
                                                          AAQ22728 standard;
                                                                                                                                                                                                                                                                                                   Sequence 6848 BP; 1848 A; 1585 C; 1873 G; 1431 T; 0 U; 111 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human soft tissue sarcoma-upregulated DNA - SEQ ID 5266.
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                                                                                                                 GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1415
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(revised)
(first entry)
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Pred. No. 0.0044;
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ADF69743; 12-FEB-2004

(first entry)

ADF69743 standard;

CDNA; 1053 BP

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Matches 103;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A human thrombocyte lambda gt 11 expression library was expressed in E. color 17090 and was screened with serum from a deratomyositis patient. This serum had previously been found to only contain anti- Mi-2 autoantibodies. A CDNA clone L1 was selected that expressed a protein which reacted with the anti-Mi-2 serum but not with the sera from normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1053 BP; 265 A; 256 C; 341 G; 191 T; 0 U; 0 Other;
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Pred. No. 0.0038;
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RESULT 25
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Matches 103
Human; prostate cancer; cytostatic; carcinogen; pharmacogenomic marker; gene; ss.
                                                                              Human prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of human antigens Mi-2 and PM-Sc1, and the polynucleotide sequences encoding them. The human Mi-2 or PM-Sc1 proteins or a portion (at least one epitope) of them may be used in assays for diagnosing dermatomyositis, polymyositis or myositis-setierosis overlap disorders. The present sequence encodes human Mi-2
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                                                                                                                                      16-SEP-2002
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                                                                                                                                                                                                                                             ABV23250 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIV OKLAHOMA.
OKLAHOMA MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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/partial
/product= "Mi-2 antigen"
/prote= "This sequence lac"
                                                                              expression marker cDNA 23241.
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                                                                                                                                                                                                                                          CDNA; 6331
                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 257
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lacks both start and stop codons"
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                         pharmacodyanamic
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RESULT 26
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Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate call carcinogenic potential of a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
Human; ss; gene; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon canc kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                Human DNA encoding
                                                                                                                                   ACD13374;
                                                                                                                                                                   ACD13374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6331 BP; 1719 A; 1551 C; 1817 G; 1233 T; 0 U; 11 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                  13-AUG-2003
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18-JUL-2000;
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25-MAY-2000;
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                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 4195-4196; 11750pp; English.
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                                                                                                                                                                                                                                                   GCTGCCCTCACTGTGAGAAGGAGGGGGGTCCAGTGGGAGGCCAAGGAGGAAGAAGA 1520
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; 2000US-0207454P.
; 2000US-0211314P.
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; 2000US-0255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.9%;
                                                                  p53 modifier,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59.8;
Pred. No. 0.
                                                                                                                                                                   ВP
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                                                                  SEQ ID 44.
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                    colon cancer;
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CC polypetide (human orthologue of genes that modify the p53 pathway in CC prosphila) or nucleic acid with a test agent under conditions, where but CC for the presence of the test agent, the system provides a reference CC activity, and detecting a test agent, biased activity of the assay system. CC Also included are modulating (M2) a p53 pathway of a cell (comprising CC contacting a cell defective in p53 function with a candidate modulator CC that specifically binds to a HM polypeptide comprising an HM amino acid CC sequence, where p53 function is restored), modulating (M3) a p53 pathway of a disease in a patient (comprising contacting the cell with an agent that CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) CC a disease in a patient (comprising: (a) obtaining a biological sample CC whether the comparison indicates a likelihood disease). (M1) is useful CC for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 ** expression level.

CC Modulators identified by (M1) are useful in a variety of diagnostic and CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation of the cell, so that the cell undergoes normal CC also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation or progression through the cell cycle. (M2) and (M3) are apoptotic or cell proliferation disorders. The present sequence is an HM CC apoptotic or cell proliferation a p53 pathway modifying pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence is an HM CC apoptotic or cell proliferation disorders. The present sequence is an HM CC apoptotic or cell proliferation disorders. The present sequence is an HM CC apoptotic or cell proliferation disorders.
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Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-2001; 2001US-0296076F
10-OCT-2001; 2001US-0328605F
15-FEB-2002; 2002US-0357253F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying (M1) a candidate p53 pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 269-271; 678pp; English
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                                                                                                                                                                                                                                                                                                                                                           103;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid encoding a p53 pathway modifying protein
GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
                                                                   GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
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llarity 58.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                           <u>,</u>
                                                                                                                                                                                                                                                                                                                                                   Score 59.8; DB 8
Pred. No. 0.0048;
0; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1240 T;
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Sequence 6331 BP;

1720 A; 1552

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G; 1240 T; 0 U; 0 Other

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                                                                  The present invention relates to antiangiogenic pharmaceutical compositions. The compositions comprise, as active ingredient, one or more of: nucleic acid (I; ADI26740-ADI26744 and ADI26766-ADI26769) from more of: nucleic acid (I; ADI26740-ADI26744 and ADI26766-ADI26769) from an endothelial cell gene the expression of which is induced by an ADI26749-ADI26799 and ADI26779-ADI26779. The compositions are used in the complement or fragment; polypeptide (II; ADI26750-ADI26773) able to inhibit expression of (I); or an antibody (Ab) that binds (II). The compositions are used for treating a wide range of angiogenic diseases: tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; are used with neovascularization; restenosis (arterial or after balloon angioplasty); overian hyperstimulation; psoriasis; endometriosis atheroscolated with neovascularization; restenosis (arterial or after balloon angioplasty); overgrowth of cells in wound healing; peripheral vascular thrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; thrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; chronic heart disease; (congestive) cardiac insufficiency; age-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                    muscular degeneration and osteoporosis. This sequence encodes chromodomain helicase DNA binding protein 3 (CHD3).
                                                                                                                                                                                                                                                                                                                                                                                                                               Antiangiogenic composition, useful for treating e.g. tumors, connew angiogenesis-related nucleic acids or related polypeptides, antibodies or antisense sequences.
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DB; ADI26773.
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211. .6045
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                     The present invention relates to antiangiogenic pharmaceutical compositions. The compositions comprise, as active ingredient, one or more of: nucleic acid (I, ADI26740-ADI26744 and ADI26766-ADI26769) from an endothelial cell gene the expression of which is induced by an angiogenic agent, or its complement or fragment; polypeptide (II; ADI26745-ADI26749) and ADI26770-ADI26773) encoded by (I), or its fragment; an antisense nucleic acid (III; ADI26750-ADI26753) able to inhibit
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                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                   Human; p53 pathway; therapeutic; angiogenic disorder; apoptotic disorder; chromodomain helicase DNA binding protein; CHD; cancer; gene therapy; cell proliferative disorder; chromatin organisation modifier domain;
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                       Disclosure;
                                                          Identifying a candidate p53 pathway-modulating targets for disorders related to defective p53 contacting an assay system having purified CHD
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15-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
                                                a test agent.
                      Page
                                                                                                                                                                                               ; 2001US-0296076P.
; 2001US-0328605P.
; 2001US-0338733P.
; 2002US-0357253P.
; 2002US-0357600P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             llarity 58.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                  Plowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                        51-54;
                                                                                                                                                                          INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1720 A; 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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                      278pp;
                                                                                                                                                  Belvin M,
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Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA binding
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                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1819
                                                                                                                                                 Francis-Lang
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72;
                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1240 T;
                                                          agent as therapeutic function e.g. cancer polypeptide or nucle:
                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                 Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding
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                                                              cancer by
                                                                                                                                                  Funke
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                                                                                                                                                  RP.
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RESULT 30
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Best Local Simi
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathway modulating agents. The method involves contacting an assay system comprising purified chromatin organisation modifier (chromo) domain helicase DNA binding proteins (CHD), nucleic acids, their functionally active fragments or derivatives, with a test agent under conditions where, but for the presence of the test agent, the system provides a reference activity. The methods are useful for identifying modulators of the p53 pathway as therapeutic targets for disorders associated with defective p53 function, such as angiogenic disorders, apoptotic disorders or cell proliferative disorders, e.g. cancer. The modulators are useful as research reagents, diagnostics and therapeutics. The invention is also useful in gene therapy. The present sequence is human CHD DNA
                                                                                                                                                                                                                                                                                                                                                                               gene therapy; antiangiogenic; tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; atherosclerosis; neovascularization; ovarian hyperstimulation; psoriasis; endometriosis; neovascularization; restenosis; cardiovascular disease; hypertension; Raynaud disease; muscular degeneration; osteoporosis; human; zing finger; helicase; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiinflammatory; Antiarteriosclerotic; Antipsoriatic; Gynaecological; Vasotropic; Vulnerary; Hypotensive; Antianginal; Cardiant; Osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; ophthalmological; Antiarthritic; Antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human GS-N3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI26742 standard; DNA; 6771 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6331 BP; 1720 A; 1552 C; 1819 G;
WPI; 2003-806304/76.
P-PSDB; ADI26747.
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                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                            22-MAR-2002; 2002FR-00003655
                                                                                                                                                                                           26-SEP-2003.
                                              Colin S,
                                                                                                                            22-MAR-2002; 2002FR-00003655
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                                                                            GENE SIGNAL.
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                                              Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence, SEQ ID 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72;
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RESULT 31

ABX 63 370

ID ABX 63 370

ID ABX 63 370

ID ABX 63 370

AC ABX 63

AC ABX 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to antiangiogenic pharmaceutical compositions. The compositions comprise, as active ingredient, one or more of: nucleic acid (I; ADI26740+ADI26744 and ADI267765-ADI26769) from more of: nucleic acid (I; ADI26740+ADI26744 is induced by an anticomposition of the expression of which is induced by an angiogenic agent, or its complement or fragment; polypeptide (II; ADI26745-ADI26749 and ADI26770-ADI26773) encoded by (I), or its fragment; an antistense nucleic acid (III; ADI26750-ADI26733) able to inhibit expression of (I); or an antibody (Ab) that binds (II). The compositions are used for treating a wide range of angiogenic diseases: tumour vascularisation; retinopathy; rheumatoid arthritis; Crohn disease; atheroscis; ovarian hyperstimulation, psoriasis; endometriosis associated with neovascularization; restenosis (arterial or after ballon angioplasty); overgrowth of cells in wound healing; peripheral vascular disease; hypertension; vascular inflammation; Raynaud disease; aneurysm; thrombophlebitis; lymphedema; ischaemia; angina; myocardial infarct; chrombophlebitis; lymphedema; ischaemia; ansufficiency; age-related muscular degeneration and osteoporosis. GS-N3 encodes a zing finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Sim
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis; ischaemia-reperfusion injury; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene; 88; vascular tissue; cytostatic; atherosclerosis; cardiant; hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antiangiogenic composition, useful for new angiogenesis-related nucleic acids antibodies or antisense sequences.
                                                                  28-JUL-2000; 2000US-0222469P.
08-JAN-2001; 2001US-0260483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA #370 differentially expressed in activated vascular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABX63370;
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                                                                                                                                                                        08-JAN-2002; 2002US-00044090
                                                                                                                                                                                                                                          26-SEP-2002.
                                                                                                                                                                                                                                                                                                         US2002137081-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59.8;
Pred. No. 0
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(BAND/) BANDMAN

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RESULT 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC antiatrerioscalerotic; cytostatic; cardiant; hypotensive; antidiabetic; cytostatic; cytostatic; cardiant; hypotensive; antidiabetic; cytostatic; cardiant; hypotensive; and may be used in gene therapy. The cDNAs of the invention may be used in a high-cytostatic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-cytostatic and compounds to the convention. A protein encoded by the cDNA may be used to screen several convention. A protein encoded by the cDNA may be used to screen several convention. A protein encoded by the cDNA may be used to screen several convention. A protein encoded by the cDNA may be used to screen several convention, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or combinant protein from a sample. The nucleotides may be useful for conjury. It also the protein gene in a sample or purify a natural or conjury. Testing, treating, or monitoring the progression of treatment conjury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid conjury, restenosis, or stroke. The cDNAs can also be used for large-scale conjury, restenosis, or stroke. The cDNAs can also be used for large-scale conjury, restenosis, or stroke. The cDNAs can also be used for large-scale conjury, restenosis, or stroke. The cDNAs can also be used for large-scale conjury, restenosis, or stroke. The cDNAs can also be used for large-scale conjury, restenosis, or stroke. The cDNAs can also be used for large-scale conjury, restenosis, or stroke. The cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases conjury. The present sequence represents a cDNA of the invention conjury and the protein format directly from USPTO at https://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim:
Matches 103;
hepatotropic; antiinflammatory; virucide; cytostatic; gene t differentially gene expression; liver; toxin; liver disorder biliary cirrhosis; X-linked adrenoleukodystrophy; Zellweger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7805 BP; 2003 A; 1945 C; 2323 G; 1534 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises geveral cDNAs that are differentially expressed in activated vascular tissue.
                                                                                                     Human liver differentially expressed cDNA seq id 400
                                                                                                                                                               22-APR-2004
                                                                                                                                                                                                                                                               ADI22590 standard; DNA; 7805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a combination comparising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandman
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                                                                                                                                                                                                                                                                                                                                                                                          GCTGCCCTCACTGTGAGAAGGAGGGGGGGTCCAGTGGGAGGCCCAAGGAAGAAGA 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          egeccirccacciecciecciecciccccccccacaeaearccccacaeaeacciega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                             (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.9%;
                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59.8; DB 8; L
Pred. No. 0.005;
"" wigmatches 72;
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                          disorder;
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WO2003000898-A1

Oryza sativa

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RESULT 33
ADA71938/c
ID ADA719
XX ADA719
XX ADA719
XX CO-NOV
XX ZO-NOV
XX Plant;
XX Plant;
XX gene;
XX Gyza
XX Oryza
XX OCO0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a combination comprising a number of cDNAs that are differentially expressed in a liver treated with a toxin and are selected from any of the 514 cDNAs listed in the specification, or their complements. The combination is useful in diagnosing, staging or treating a liver disorder (e.g. billary cirrhosis, x-linked adrenoleukodystrophy, Zellweger syndrome, hepatorenal syndrome, hepatitis or hepatocarcinoma), in monitoring diagnostic and therapeutic applications, in detecting metabolic and toxicological responses, and in elucidating drug mechanism of action. This sequence represents a cDNA differentially expressed in liver tissues in response to treatment with a toxin.
                                                                                                                                                                                                                                                                                                                               ADA71938 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7805 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New combination comprising a number of cDNAs that are differentially expressed in a liver treated with a toxin, useful for diagnosing, story treating liver disorders (e.g. biliary cirrhosis, hepatitis or
                                                                                                                             Plant; bacterial
                                                                                                                                                                          Rice gene,
                                                                                                                                                                                                                                                                                ADA71938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cunningham MJ, Kaser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatorenal syndrome; hepatitis; hepatocarcinoma; metabolic response; toxicological response; ss; EST; expressed sequence tag; human.
                                                                                                                                                                                                                              20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000; 2000US-0251986P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-2001; 2001US-00006285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CUNN/) CUNNINGHAM M J. (KASE/) KASER M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1690
                                                                                                        ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGCCCTCACTGTGAGAAGGAGGGGGGTCCAGTGGGAGGCCAAGGAAGAAGAAGA 1804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCCGGGCAGAGGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
                                                                                                                                                                            SEQ ID 5263
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                                                                                                                                                                                                                              (first entry)
                                                                                                                             infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003 A; 1945 C; 2323 G; 1534 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                               DNA;
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                                                                                                                             fungal infection; viral infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-2001; 2001WO-IB001105
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                                                                                                                                                      GCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCT
                                                                                                                                                                                                                                                                                                               TMYTTSRSRMMYTGRYKARYTSKRRYMWYKYRKYCWYYYYGMYMKCSYMMRYGYCKACKK 481
                                                                                                                                                                                                                                                                                                                                                                          MTCTMYTSMKGSTRRSKWGRWSGMSRMYMRWWKKMRKRKYMRYMKWKCTWRRCMCYRWGY
                                                                                                                                                                                                                                                                                                                                                                                                                                         SCWMYWRGARSMWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCG
                                                                                                                                                                                                                   CCYAMCWKAAYSGMMYWYRKYSKWMRMSTKYMWSMW-----YKKCRSMKYGAKGCYGCK
                                                                                                                                                                                                                                                                              CCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTGCGCGTTGCGGGG
                                                                                                                                                                                                                                                                                                                                          ACCTGCCGGCTCCGCCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTGCACC
                                                                                                                                                                                                                                                                                                                                                                                                         AGGTAAGAGGTCCACCTGGGGAACCCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGC
WSRSAAKRTYKGYSTSRRÄKMMRÁCRMYSÁCRRYSRTSYYCGCSYCGSSKWKYMSKSCSM
                           CCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACC
                                                                                          CAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCCAGCCCCGCCCCGCCTGG
                                                                                                                       KYWYKRRGTMSWYGKSYKKKYCTWWCYMKCMRCYRWRKMMRKKTKYSKRCYCWRYATCYW
                                                                                                                                                                                     MWTYCSYGYMKWYTYMGSYKYSRCYKYMR-MYMYKGWMYMMYYSAYSSMMTWYYYYAKYW
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F, Quan
                                                            CCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKMYKKMWKKSYYMSYGWARSSGT
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S, Tao Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338; Mismatches 290;
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Pred. No. 0
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ie Z,
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary carcinomas e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary assoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1997;
09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX53491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSRWMSMYYAAKMGMCGSSGMYRMSKSCKMYSKYSSCKYTGSKKCTKRKYYYCYWSSG
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Query Match
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                                                                                                                                                                                NDNNCCGCBGGCCBSNNNDNNCCGCBGGCCSNNNDNNCGCBGGCCBGGCGCGCCGCCG-
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                                                                                GCCGGGCCGSNNNDNNGCBGGCCBGGGCGCGCCGCCGGCCGGGCCGSNNNDNNCBGGCCB
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6124 BP; 1706 A; 1562 C; 1509 G; 1347 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 21665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid
genes from Drosophila and
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11-JUL-2000;
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             TGGAGGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTG
                                                                                                                                                                                                                                                                                         AACGAGGACTGGTGCGCCGTCTGTCTGGATGGAGGCGAGCTGATGTGCTGCGACAAGTGT
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                                                                                                              rCCATCAGAACTGTCACATCCCTGCGATCAGCTCGTTGCCGGACGAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
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ABL09060
                                                                                                                                                                                         Matches
                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-BB130511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                     Sequence 21747 BP; 6181 A; 4697 C; 4637 G; 6232 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 21662; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE
                                                                                                                                                                                                        Local Similarity
17930
                                                                                                                           17810
                               648
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)B; ABB64957.
                                                                                                                                                           528
                                                                                                                                                                                          96;
                                                                                                                                               AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC 587
GAGAGCTGGCAGTGCCTACTGTGCGTCAACATCAAGGAGCTG
                            TGGAGGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTG
                                                            CCCAAAGTTTTCCATCAGAACTGTCACATCCCTGCGATCAGCTCGTTGCCGGACGAGAGC
                                                                                 CCTCGGGCCTTCCACCTGGCCTGCCTGCCCTCCGGGAGATCCCCAGTGGGACCC
                                                                                                                           AACGAGGACTGGTGCGCCGTCTGTCTGGATGGAGGCGAGCTGATGTGCTGCGACAAGTGT 17869
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                                                                                                                                                                                          Conservative
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                                                                                                                                                                                         66;
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                            689
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                                                            17929
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gxg

ACH90409;

Query Match Best Local Similarity

3.6%; 48 C;

Score 55.4; Pred. No. 0.

Length 153;

153

B₽; 29 P,

43 G; 33

T; 0 U; 0 Other DB 12; .025;

ACH90409/c RESULT 37

ACH90409 standard; DNA; 153 BP

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The invention relates to a nucleic acid probe for measuring human gene cappression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and concoding at least 8 amino acids of any of the 6888 amino acid sequences of fully defined in the specification. The probe is a single exom probe that thybridises under high stringency conditions to a nucleic acid molecule carpressed in human cells or tissues. Also included are a spatially-carpressed in human cells or tissues. Also included are a spatially-carpressed din human cells or tissues. Also included are a spatially-carpression (comprising a plurality of probes for measuring human cell sort measuring human gene expression, a method of gene expression (comprising a plurality of single exon nucleic acid molecule contiguous and acids of any of the plurality), a single exon microarray for measuring human gene expression, a method of sequences (optionally with conservative amino acid substitutions), an contiguous amino acids of any of the above-mentioned amino acid sof any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an ethods of selling and/or licensing single exon probes or microarrays to carpression data by subscription, and a computer-readable carpression data by subscription, and a computer-readable carpression analysis. The probes may be used as troals for surveying tissues to detect the presence of expressed messages that contain their cartials are probe. The probes may be used as troals for surveying cated above. The probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing events, in priming the synthesis of nucleic acids, car in expressing the ORF-encoded peptide. The present sequence is a human cated care and characterising dross alternation calterations, in priming the synthesis of nucleic acids, car in expressing the order to the probes of the printed 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 23604; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                    seqdata.uspto.gov/sequence.html?DocID=20030194704
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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RESULT 38
ACH76709/c
ID ACH767
XX ACH767
XX ACH767
XX ACH767
XX ACH767
XX Human;
XX Human;
XX Human;
XX ACH767
XX AC
CC expression, comprising any of the 27,400 fully defined nucleoride CC sequences in the specification, or their complements or fragments, and CC encoding at least 8 amino acids of any of the 6888 amino acid sequences CC fully defined in the specification. The probe is a single exon probe that CC hybridises under high stringency conditions to a nucleic acid molecule CC expressed in human cells or tissues. Also included are a spatially-CC addressable set of single exon nucleic acid probes for measuring human CC gene expression (comprising a plurality of single exon nucleic acid CC probes cited above, where each of the plurality of probes is separately CC and addressably isolatable or amplifiable from the plurality), a single CC measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an CC isolated antibody that binds specifically to a peptide cited above, comprising to measure gene expression, a method of providing the solution of selling and/or licensing single exon probes or microarrays to control of selling and/or licensing single exon probes or microarrays to control of the expression and a computer-readable
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ing event; genomic alteration.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                   New isolated polynucleotide and encoded polypeptides, udiagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and trained to the second seco
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23-AUG-2000; 2000US-00649167
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food supplement; medical imaging; diagnor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forensic;
                                                                                                                                             mutations
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Claim 1; SEQ ID

NO 18134; 103pp; English

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AAS74874
ID AAS7
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      RESULT 40
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Best Local S
Matches 86
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; sood supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #10678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS74874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS74874 standard; cDNA; 7132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2495 BP; 696 A; 581 C; 733 G; 485 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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New isolated polynucleotide and encoded polypeptides, useful in
                                                               P-PSDB; ABG10687.
                                                                                           WPI; 2001-639362/73
                                                                                                                                                                                                                (HYSE-) HYSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         supplement;
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                                                                                                                                                    ΡΤ,
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                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                    Tang
                                                                                                                                                       Ϋ́
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies and the states involving (III). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in effective in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                  Sequence 7132 BP; 1723 A; 1875 C; 1964 G; 1569 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention
                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
1487
                                                                                                                                                                                 1367
                                                                                                                                                                                                      532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
                                                                                                                                   592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                                            86;
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                              AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
GCTGCCCACACTGCGTG 1503
                                        GGTGCTCCAGCTGCCTG 668
                                                                                      GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is useful
                                                                                                                                                                                                                                                                                             3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as hybridisation probes,
                                                                                                                                                                                                                                                                       Score 55.4; DI
Pred. No. 0.04:
0; Mismatches
                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                 .042;
                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                     Length 7132;
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                                                                                                                                                                                                                                                                            Gaps
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                                                                                           1486
                                                                                                                                      651
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RESULT 41 AAK71358 31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; Human; immune; haematopoietic; immune/haematopoietic antigen; cancer cytostatic; gene therapy; vaccine; metastasis; ds. AAK71358 standard; DNA; 37314 BP 17-JAN-2001; 2001WO-US001354 cytostatic; gene 06-NOV-2001 09-AUG-2001. WO200157182-A2 immune/haematopoietic antigen genomic sequence SEQ ID NO:26170. 2000US-0179065P. 2000US-0180628P. 2000US-0184664P. 2000US-0186350P. 2000US-0189874P. (first entry) therapy; vaccine;

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13-OCT-2000
20-OCT-2000
20-NOV-2000
20-NOV
                                                                                               Nucleic
useful f
AAK54951 to AAK64702 amino acid sequences activity, and can be
                                                               Disclosure;
                                                                                                                                               2001-483426/52.
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                                                                                               for
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                                                                                                                                                                            Barash
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2000US-0241969P
2000US-0241785P
2000US-0241808P
2000US-0241808P
2000US-0246476P
2000US-0246476P
2000US-0246476P
2000US-0246523P
2000US-0246523P
2000US-0246523P
2000US-0246523P
2000US-0246523P
2000US-0246526P
2000US-0246528P
2000US-024651P
2000US-024651P
2000US-0249211P
2000US-0249219P
2000US-02511866P
2000US-02511866P
2000US-02511899P
2000US-0251989P
                                                                                                                                                                                                               GENOME
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                                                                                                                                                                            SC,
                                                             ĕ
encode the human immune/haematopoietic antigen (I) given in AAM82170 to AAM91921. (I) have cytostatic used in gene therapy and vaccine production. (I)
                                                                                                                                                                                                               SCI
                                                               26170; 3071pp +
                                                                                             human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                             Ruben
                                                                                                                                                                               SM;
                                                               Sequence Listing;
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antigen

polypeptides, and metastasis.

English.

17. MAR - 2000
19. MAY 2000
19. MAY 2000
20. JUN 2000
20. JUN 2000
21. JUN 2000
21. JUN 2000
22. JUN 2000
14. AUG 2000
15. SEP 2000
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2000US-0190076P.
2000US-020551BP.
2000US-021513BP.
2000US-0216647P.
2000US-021513BP.
2000US-021513BP.
2000US-021748F.
2000US-021748F.
2000US-021748F.
2000US-021748F.
2000US-022551BP.
2000US-022551BP.
2000US-022551BP.
2000US-0225758P.
2000US-0225758P.
2000US-0225767P.
2000US-0225768P.
2000US-0225768P.
2000US-0225768P.
2000US-0225768P.
2000US-0225768P.
2000US-0225768P.
2000US-022578BP.
2000US-022578BP.
2000US-022578BP.
2000US-0231244P.
2000US-0231244P.
2000US-0231244P.
2000US-023144P.
2000US-023146P.
2000US-023146P.
2000US-023168P.
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2000US-023168P.
2000US-0231703P.
2000US-023703P.
2000US-023703P.
2000US-023703P.
2000US-02337049P.
2000US-023703P.
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2000US-023703P.
2000US-0233704P.
2000US-023703P.
2000US-0233704P.
2000US-023703P.
2000US-023703P.
2000US-023703P.

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RESULT 42
ABQ88207/c
ID ABQ882
XX ABQ882
XX ABQ882
XX ABQ882
XX OSTEOD
DT 18-SEP
XX OSTEOD
XX OS
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Best Local S
Matches 86
                                                                                                                                       Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2000; 2000US-0255882P
24-APR-2001; 2001US-0285691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; osteoblast; stem cell differentiation; bone tissue deposition; osteoporosis; osteopathic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human osteoblast differentiation related cDNA SEQ ID NO 114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ88207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2001; 2001WO-US048276
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                                                                                                                                                                                                                                                                                                  WPI; 2002-557663/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7106
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                                                                                                                                                                                                                                                                                                                                                                                                              Axelrod DW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              Cook JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          Jaiswal N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ЧВ
                                                                                                                                                                                                                                                                                                                                                                                                          Einstein R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
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                                                                                                                                                                                                                                                                                                                                                                                                          Houghton
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Claim 1; SEQ ID NO 114; 78pp + Sequence Listing; English

(GEMY ) GENETICS INST INC

98US-0104436P

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RESULT 43
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ID AAA45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The invention relates to genes and their expression profiles are used CC for: (ā) screening modulators of precursor stem cell differentiation into CC osteoblasts, or bone tissue deposition; (b) diagnosing abnormal CC deposition of bone tissue, abnormal rate of osteoblast formation or CC cited in (b), or monitoring the progression of bone tissue deposition. Specific conditions include postunenchausal osteoporosis, glucocorticoid CC osteoporosis or male osteoporosis, osteoporosis, glucocorticoid CC induced abnormalities in bone formation or bone loss, conditions that induced abnormalities in bone formation or bone loss, conditions that CC involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), CC skeletal disease linked to breast cancer, mastocytosis, Panconi syndrome CC or fibrous dysplasia. The present sequence is that of an osteoblast CC differentiation associated cDNA marker of the invention. Note: The CC sequence data for this patent did not form part of the printed constitutions in the printe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                    expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; vaccine; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; mouse; chicken; rat; secreted expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 172570 BP; 45194 A; 43991 C; 41126 G; 42258 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse secreted expressed sequence tag SEQ ID NO:1940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA45365 standard;
                                                                                                                                 L5-OCT-1999;
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                                                                                                                                    99WO-US024206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55.4;
Pred. No. 0
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RESULT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antivivral; antidiabetic; antiasthmatic; vulnerary; antiulcer; cerebroprotective; notropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the sESTs. Proteins encoded by the sESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45936 to AAA45931 represent linker variants which are given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 93
                                                                                                                                                                                                               Human lung tumour cDNA #453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders.
                                                                                                                                                                                                                                                       13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 523 BP; 134 A; 113 C; 167 G; 96 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags (8ESTs), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 695; 803pp; English.
                                      17-APR-2003
                                                                         US2003073623-A1
                                                                                                                                                                                                                                                                                                                                ACH48320 standard; cDNA;
30-JUL-2001; 2001US-00918995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
                                                                                                                                                  ss; sequencing by hybridisation; SBH; expressed sequence tag; mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGACGAGTGTGCCGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%;
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                                                                                                                                                                                                                                                                                                                                    494
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687
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                                                                                                                                                 Query Match
Best Local S
Matches 86
                                                                                                                                                                                                  included is a purified polymeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                 Sequence 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LABA/)
(STAC/)
(DICK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polymucleotide comprising any one 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antisense DNA
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                                                                                                                                                                                    seqdata.uspto.gov/sequence.html?DocID=20030073623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence watermined by the technique of SBH (sequencing by hybridisation). Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DRMA/)
 109
                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LABAT I.
STACHE-CRAIN
DICKSON M C.
JONES L W.
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 35532; 44pp; English.
                                                                         Conservative
                                                                                                                                                 BP; 154 A; 101 C; 102 G; 136 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or RNA.
                                                                                         3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stache-Crain
                                                                         0;
                                                                         Score 54.2; D
Pred. No. 0.05
0; Mismatches
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                                                                                           .053;
                                                                                                          DB 9;
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                                                                                                            Length 494;
                                                                         Indels
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RESULT 45
ADB80995
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                                                                                         04-DEC-2003
                                                                                                                                ADB80995 standard;
                                                                                                            ADB80995;
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                                                                                                                                                                                                                                                                             AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                                                               ATGAGGACTGGTGTGCAGTTTGTCAAAACGGAGGGGAACTCCTCTGCTGTGAAAAGTGC
                                                                                                                                                                                  TGGATTTGCACTTTCTGCC
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                                                                                                                                                                                                   TGGAGGTGCTCCAGCTGCC
                                                                                         (first
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                                                                                         entry)
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RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60; Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsg cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;

tsg101;

RING-SH complex related

DNA,

SEQ ID

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3039 BP; 941 A; 738 C; 664 G; 696 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated protein complex comprising a RING-SH 3 polypeptide and another polypeptide, useful for detecting cells infected with a virus, and for treating viral disorders caused by retroviruses, rhabdoviruses
                                                                                                                       Human cDNA differentially expressed in MYCN activated cells SeqID 284
                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                ADJ56478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greener T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001; 2001US-0308958P.
09-NOV-2001; 2001US-0345846P.
                                                                             human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy
                                                                                                                                                                                                          ADJ56478 standard; cDNA; 3917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 68; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-2002; 2002WO-US024589
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              US2003119009-A1
                                        Homo sapiens
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                                                                    activated
                                                                                                                                                                                                                                                                                                        648
                                                                                                                                                                                                                                                                                                                                                                                                                                                 96;
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                                                                                                                                                                                                                                                                                                                                                                                          AATGAGGACTGGTGTGCAGTTTGTCAAAACGGAGGGGAACTCCTCTGCTGTGAAAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                     AATGAGGACGAGTGTGCCGTGTGTCGGGAACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                                                                                                        recaecrecrecaecrece 666
                                                                                                                                                                                                                                                                                                                                    CCCAMAGTATTCCATCTTTCTTGTCATGTGCCCACATTGACAAATTTTCCAAGTGGAGAG
                                                                                                                                                                                                                                                                              TGGATTTGCACTTTCTGCC 2497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                   (first
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                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54.2; DB Pred. No. 0.068;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
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                                                                              gene therapy; ss
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           Homo sapiens
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RESULT 47
AAK94864
ID AAK94
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Best Local S
Matches 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the concerns of the cancers.
Human; full length
                                     Human
                                                                          06-NOV-2001
                                                                                                                                                AAK94864 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3917 BP;
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                                                                                                               AAK94864;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-2001; 2001US-0270784P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-2002; 2002US-00084817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      printed specification but has been obtained in electronic format US Patent Office at
                                                                                                                                                                                                                                            2479
                                                                                                                                                                                                                                                                                                                    2419
                                                                                                                                                                                                                                                                                                                                                                                             2359
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                                                                                                                                                                                                                                                                                                                                                                                                                              528 AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
                                     full-length cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
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NUCHTERN J G.
PLON S E.
SHOHET J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                        CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 284;
                                                                                                                                                                                                                                            TGGATTTGCACTTTCTGCC 2497
                                                                                                                                                                                                                                                                               TGGAGGTGCTCCAGCTGCC 666
                                                                                                                                                                                                                                                                                                                    CCCAAAGTATTCCATCTTTCTTGTCATGTGCCCACATTGACAAATTTTCCAAGTGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                             AATGAGGACTGGTGTGCAGTTTGTCAAAACGGAGGGGAACTCCTCTGCTGAAAAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1232 A; 863 C; 843 G; 979 T; 0 U; 0 Other;
cDNA; cDNA synthesis; oligo-capping;
                                                                                                                                                CDNA; 3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%;
                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27pp;
                                   SEQ ID NO: 4044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54.2; DB Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53,
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 88
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RESULT 48
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Matches 86
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
                                                    EP1396543-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3997 BP; 1221 A; 944 C; 911 G;
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                                                                                                   Homo sapiens
                                                                                                                                                    oligo-capping
                                                                                                                                                                                                                           Full length human
                                                                                                                                                                                                                                                                               20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                ADL32011 standard;
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  10-MAR-2004
                                                                                                                                                                         human; medicine; signal transduction; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGAGGACGAGTGTGCCGTGTGTCGGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAGGTGCTCCAGCTGCC 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCTCCGGGAGATCCCCAGTGGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCAAAGTATTCCATCTTTCTTGTCATGTGCCCACATTGACAAATTTTCCCAAGTGGAGAG
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2000JP-00183765
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                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                               method; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiyama
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                                                                                                                                                                                                                           cDNA clone SeqID 4044.
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a T, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1380pp + Sequence Listing; English.
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Pred.
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K, Kojima
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No. 0
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S, Otsuki
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                                                                                                                                                                         transcription;
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. T, Koga
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RESULT 49
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tength cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
                                                                                                         Antisense oligonucleotide; multiple target; antisense treatm impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                     pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; colon cancer; backetic cancer; cancer; cancer; pancreatic cancer; bepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                 Human adenosine Al receptor antisense oligonucleotide
                                                                                                                                                                                                                                                        AAX53491;
                                                                                                                                                                                                                                                                                   AAX53491 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligonucleotide primers length human cDNAs.
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                                         prostate cancer;
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DB; ADL32012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCGGGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATCCCCCAGTGGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 99JP-00194486.
; 2000JP-00118774.
; 2000JP-00183865.
; 2000EP-00114089.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
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                                                                                                                                                                                                                                                                                   DNA;
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na T, Nagai
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Pred. No. 0.07:
0; Mismatches
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K, Kojima
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T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 37; 120pp; English.
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                                                                                                                                                                                                                                                                                                          GCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCGGCCCCAGGAGCCACC
                                                                                                                                                                                                                                                                                                                                               GGGCCGAGCCAGGGGCCCNNHNNNSVGCGGAGCCVGCGCCCNNHNNNSCGGCCCGGCCNN 105480
GGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTGCGGGGTTGCGGGGGTGTGCGGAGATGGT
                                                        GTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114955 BP;
                                                                                                                               TGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGCACCTGCCGGCTCCGCC
                                                                                                                                                                                                   CNNHNNNSCGGCCCGGCCGGCGGCGCNNHNNNSCGG
                                                                                                                                                                                                                                      CGTGGAGACCCCCCCCCCCCGGGGCTTAGGTCGGCGGAGAGGAGGTAAGAGGTCCACC
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98US-00093972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54;
Pred. No.
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RESULT 50
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30-JUN-2000;
03-AUG-2000;
The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging of the probes are therefore useful in grading and/or staging the problem and the problem are the problem and the problem are the problem and the problem and the problem are the problem are the problem and the problem are t
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                                                                                                                                                                                                                                                                                                                                 2001-488901/53.
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                                                                                                                                                                                           SEQ ID NO 15023; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-0207456P.
; 2000US-0068408.
; 2000US-00632366.
; 2000US-02334687P.
; 2000US-0236359P.
; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104806
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                                                                                                                                                                                                                                                                                                                                                                                          Rank
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RESULT 51
ABA70776/c
ID ABA70776/c
ID ABA7077
ACC ABA707
XX ABA707
XX Human;
XX Human;
XX Human;
XX Homo &
XX Homan
PT Gene Note:
CC Ine i
CC Homan
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CC Segue
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases of the cervix, notably cervical cancer. for this patent did not form part of the printed obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences
                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA70776 standard; DNA; 292
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                              ftp.wipo.
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    292
                                                                                                                                                              SEQ ID NO 19081; 639pp + Sequence Listing;
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                           int/pub/published_pct_sequences
    BP;
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   94 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon nucleic acid
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   67 G;
                                                                                                                                                                                                                                                                       Rank DR;
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   T; 0 U; 0 Other;
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                                                                                                                                                              English
                                                                                                                                                                                                            for
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RESULT 52
AAI50949/c
ID AAI509
                                       Query Match
Best Local Similarity
Matches 84; Conserv
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Best Local Similarity
Matches 84; Conserv
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26-MAY-2000; 2000US-0207456F.
30-JUN-2000; 2000US-0008408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                      The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders
                                                                                               Sequence
                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000663
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                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                             expression
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                                                                                                                                                                                                                                            genome-derived single exon nucleic expression in human placenta.
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ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCC
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                                                                                                                                                                                                                  SEQ
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                                        Conservative
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                                       Score 52.8; Di
Pred. No. 0.09
0; Mismatches
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Pred. No. 0.09;
0; Mismatches
                                                                                               67 G; 66 T; 0 U; 0 Other;
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ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGTGATACCTGTC

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                                                                                                                          RESULT 53
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                                                               Query Match
Best Local S
Matches 84
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                              measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                       Sequence 292 BP; 65 A; 94 C; 67 G; 66 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA37266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA37266 standard; DNA; 292
                                                                                                                                                                                                                                                                                                                               Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2002
                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #15732
                                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
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                                                                                                                                                    directly
                                                                 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                            SEQ ID NO 15732; 530pp; English.
         ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGTGATACCTGTC
                                    ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGAGCTCATCTGCTGTGACGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTCTGTCCCCGTTG 5
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                                                                 Conservative
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                                                                                                                                                    from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                           3.4%;
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                                                               Score 52.8; DB
Pred. No. 0.098;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
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RESULT 54
AAK44980/c
ID AAK449
XX AAK449
XX AAK449
XX Human
XX Human;
KW Human;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                      Sequence 292 BP; 65 A; 94 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow expressed exon; gene microarray; cancer; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK44980 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                          the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed single exon probe SEQ ID NO: 19537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
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     649
                                                                                                                                                                                               529 ATGAGGACGACTGTGCCGTGTGTCCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
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                                                                                                                                                                                                                                                                    84;
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                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                          CTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCT
                                                                                                                                                              ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGTGATACCTGTC
     GGAGGTGCTCCAGCTG 664
                                                         CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCCAACGGTGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 19537; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                    Conservative
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2000US-00632366.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000US-0024263.
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                                                                                                                                                                                                                                                                                       Score 52.8;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                   67 G;
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                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                               . 098;
                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancers sequence is one of
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RESULT 55
AAK19029/C
ID AAK19029/C
ID AAK190
AC AACT
AC AAK190
AC AACT
AC AA
RESULT 56
ABS44646/c
ID ABS446
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Matches 84
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention provides a number of single exon nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                   GGAGGTGCTCCAGCTG
                                                                                                                                                                                                                                             CTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCAGAATCCCCAGTGGGACCT
                                                                                                                                                                                                                                                                                                              ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGTGATACCTGTC
                                                                                                                                                                                                                                                                                                                                                          ATGAGGACGAGTGTGCCGTGTGTCGCGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
                                                                                                                                                                                                                  CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT
                                                                                                                      GGCTCTGTCCCCGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 19020; 650pp + Sequence Listing; English
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; 2000US-00608408.
; 2000US-00632366.
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; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                             3.4%;
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                                                                                                                                                                   664
                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.8; D)
Pred. No. 0.09;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               .098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 292;
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ABS44646 standard;

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Matches 84
                                                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be used for or diseases such as cirrhosts, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABSS5011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease; ss.
                                                                                                                                                                                                                     Sequence 292
                                                                                                                                                                                                                                                             sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from W
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 19636; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
21-SEP-2000;
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                           GGAGGTGCTCCAGCTG 664
                                                      CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT
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2000US-0207456P.
; 2000US-02608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000US-00024263.
                                                                                                                                                                 Conservative
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                                                                                                                                                                           Score 52.8;
Pred. No. 0
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19-AUG-2002 (first of the control of the case of the control of the case of the complements of the complements of the complements of the complement of the complements of the complem
CC probes. Also included are a microarray comprising the novel set of probes c; the novel set of probes which hybridise at high stringency to a nucleic clearly edited from human lung; measuring gene expression in a sample cd derived from human lung, comprising the array with a collection of detectably labeled nucleic acids derived from human lung congrising (a) contacting the array with a carray; identifying exons in a eukaryotic genome, comprising (a) considered nucleic acids from eukaryotic genome, comprising (a) considered nucleic acids from eukaryote lung mRNA, to a single exon probe, comprising a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the combes/open reading frames (ORF). The probes are used for gene expression comprises and the string of the exons in the tissues are used for gene expression comprises that the comprise are used for gene expression comprises that the sequence of the comprision of the exons in the tissues are used for gene expression comprises that the sequence of the comprise that the sequence of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spatially-addressable set of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000US-00024263.
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XX Probe;
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PR W02001
XX 09-AUG
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XX 13-JAN
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PR 26-MAY
PR 30-JAN
XX 04-FEB
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #5806 for gene expression analysis in human cervical cell sample
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

The present (SENP). The

invention relates to human single exon nucleic acid probes present sequence is one such probe. The SENPs are derived

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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359P.
04-OCT-2000; 2000GB-00024263.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring ar displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed
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at ftp.wipo.int/pub/published_pct_sequences
               The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                          diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                             ng gene
                                                                                                                                                                                                                                                                                                                                                                              sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                           (SENP).
                             useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         588
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Query Match Best Local Similarity Matches 84; Conserv

Conservative

0 Score Pred.

3.4%;

52.8; No. 0.

BB

4. 52;

Length 476;

Indels

0

Gaps

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RESULT 61
ABA27360/c
ID ABA27360 standard; D)
XX
AC ABA27360;
XX
AC ABA27360;
XX
PDT 23-JAN-2002 (first |
DT 23-JAN-2001 |
EXX
Human; gene expression
XX
Human; gene expression
XX
Human; gene expression
XX
Human; gene expression
XX
Homo sapiens.
XX
PD 09-AUG-2001; 2001W0-
XX
PP 30-JAN-2001; 2001W0-
XX
PP 26-MAY-2000; 2000US-
PR 26-MAY-2000; 2000US-
PR 30-JUN-2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
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Query Match
Best Local S
Matches 84
                                                                                                                                                measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; gene expression; heart; microarray; vascular syste cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428
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  84;
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCGGGCCTTCCACCTGGCCTGCCTGTCCCCCTCCGGGAGATCCCCAGTGGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGGAACTGCTCTGCTGTGATACCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTCTGTCCCCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2000US-0180312P.
2000US-0207456P.
2000US-00608409.
; 2000US-00632366.
; 2000US-0234687P.
2000US-0236359P.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                      131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5826; 530pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 476
                        3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                      A; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes
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Score 52.8; D
Pred. No. 0.1;
0; Mismatches
                                                                                                      C; 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for analyzing gene expression
                                                                                                      G; 110
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                                                 DB 4;
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                                                                                                      0 U;
  52;
                                                 Length 476;
                                                                                                      0 Other;
  Indels
0
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Gaps
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RESULT 62
AAK31915/c
ID AAK319
XX AAK319
XX Human
XX Human;
KW Human;
KW Microa
XX Homo 8
XX Homo 9
XX Homo 9
XX Homo 1
XX Hom
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                                                                                                                                                 Matches
                                                                                                                                                                               Query Match
Best Local :
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                        Sequence 476 BP; 131 A; 132 C; 103 G; 110 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK31915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome-derived single exon nucleic acid
                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                           lymphoma,
bes of the
                                                                                                                                                                                 Similarity
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                                                                                                   ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCC
cressectrocaectrocererecterecentesecresses
                                                   ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTGTGTGATACCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6472; 658pp + Sequence
                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                             invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                            3.4%;
                                                                                                                                                                                                                                                                                                                                      leukaemia and myeloma. The present sequence
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                                                                                                                                                                               Score 52.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               뮸;
                                                                                                                                                                                                          ВG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listing;
                                                                                                                                                      52;
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                                                                                                                                                                                                    Length 476;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
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                                                                                                                                                                                                                                                                                                                                      is one
                                                                                                                                                                                                                                                                                                                                                              of cancers
                                                                                                                                                      Gaps
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                                                   369
                                                                                                      882
  648
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음 성

589 368

CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT

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RESULT 63
AAKO6255/c
ID AAKO62
XX AAKO62
XX AAKO62
XX Human
DE Human
XX Human;
KW Alzhei
KW SB.

OS Homo E
XX WO2001
XX WO2001
XX WO2001
XX O4-FEE
PR 26-MAN
PR 03-AUC
PR 21-SEI
PR 27-SEI
PR 27-SEI
PR 27-SEI
PR 27-SEI
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Best Local S
Matches 84
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic
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308
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                                                                                                                                                                                                                                                                                                                                           Similarity
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  GGCTCTGTCCCCGTTG
                                              GGAGGTGCTCCAGCTG
                                                                                                  CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT
                                                                                                                                                      cTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCGAGAGATCCCCAGTGGGACCT
                                                                                                                                                                                                          ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGGAACTGCTCTGCTGATACCTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 131
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                                                                                                                                                                                                                                                                                                          Pred. No. U.1;
); Mismatches
                                                                                                                                                                                                                                                                                                                                         Score 52.8; DI
Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                    BB
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RESULT 64
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Best Local Similarity
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 476 BP; 131 A; 132 C; 103 G; 110 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression in human adult liver.
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                                  649
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GGAGGTGCTCCAGCTG
                                                                                                                                                                                                                                                ATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCC
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                                                                                          CTTCTTCCTACCACATCCACTGCCTGAATCCCCCACTTCCAGAGATCCCCAACGGTGAAT
                                                                                                                                            CTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAAGATCCCCAGTGGGACCT
                                                                                                                                                                                                             ATATGGAATTCTGTCGGGTCTGCAAGGATGGTGGGGAACTGCTCTGCTGATACCTGTC
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                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 0.1;
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GGCTCTGTCCCCGTTG 293

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The invention relates to a spatially-addressable set of single exon convenience and probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 complements or the 1287 open reading frames derived from the 12614 complements or the 1287 open reading frames derived from the 12614 complements or the 1287 open reading frames derived from the 12614 complements of the look of the look of the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample conflection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a conflection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a conflection of detectably labeled nucleic acids derived from human lung comprising (a) dependence of the enterprise and (b) measuring the label detectably bound to each probe of the carray; identifying exons in a eukaryotic genome, comprising (a) contacting the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, and (b) measuring the exons assigning exons to a single exon probe in the exone and (b) measuring the exons genomic sequence by the method conversing (a) identifying exons from genomic sequence by the method conversing (a) identifying exons from genomic sequence by the method conversing (a) identifying exons from genomic sequence by the method conversing (a) identifying exons from genomic sequence by the method conversing having a probe with the exon, where a common pattern of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene, a peptide comprising one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-02608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; hermansky-Pudlak syndrome; sarcoidosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary cyllary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS06677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 6668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          measure gene expression in human lung samples.
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RESULT 66
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Best Local S
Matches 84
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent

invention

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Claim 1; SEQ ID NO 40420; 21pp + Sequence Listing; English

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                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
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genes from Drosophila
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABL72072). The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ99469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7303 BP;
                                                   Claim
                                                                                                  New isolated polynucleotide, useful in research, diagnostic therapeutic methods, e.g. preventing or treating disorders i aberrant protein expression or biological activity.
                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal infection; autoimmune disorder; coagulation disorder; nootropic; antiallergic; antiinflammatory; immunosuppresestive; neuroprotective; cyrootatic; haemostatic; virucide; antihacterial; fungicide; immunostimulant; cerebroprotective; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; expressed sequence tag; EST; chromosome 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human coding sequence SEQ ID 202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ99469;
                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000; 2000US-00714936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-2001; 2001WO-US042950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200259260-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                        WPI; 2002-590824/63.
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                                                   ۲.
                                                                                                                                                                                                               ABP64883.
                                                                                                                                                                                                                                                                                                                                                                         HYSEQ
                                                                                                                                                                                                                                                                                         Xue AJ,
                                                      SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA; 4653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGAGCACCAG 5318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTGCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCGCTCCGGGAGATCCCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGAGCCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCA
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                                                                                                                                                                                                                                                                                                                     Goodrich
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                                                                                                                                                                                                                                                                                                                                                                         INC.
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                                                                                                                                                                                                                                                                                       Yang
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                                                   202;
                                                                                                                                                                                                                                                                                                                     RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%;
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                                                 394pp;
                                                                                                                                                                                                                                                                                                                     Liu
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Pred. No. 0
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                                                   English
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                                                                                                                                                                                                                                                                                                                     Zhou P,
                                                                                                                                                                                                                                                                                            P, Asundi V,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 15;
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involving
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                                                                                                                                                                                                                                                                                                                       Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                     QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            581
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present invention

relates to novel

human coding sequences (ABQ99268-

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RESULT 69
ABV44220
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Best Local S
Matches 76
                                                                                                                 17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides and proteins are useful for preventing, treating or ameliorating disorders involving aberrant protein expression or biological activity, e.g. haematopoletic disorders, central/peripheral nervous system diseases, mechanical and traumatic disorders, non-healing wounds, immune deficiencies and disorders, infectious diseases caused by viral, bacterial or fungal infection, autoimmune disorders, allergic reactions and conditions, coagulation disorders, or cancer. The polynucleotide sequences of the invention were assembled from ESTs isolated mainly by sequencing by hybridisation, and in some cases, sequences obtained from one or more public databases. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides are useful in diagnostics as expressed sequence tags (BSTB) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutic, diagnostic and research methods. The polynucleotides may be used in the field of molecular biology as hybridisation probes, primers for CR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABV44220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV44220 standard; cDNA; 539
Schlegel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-2002
                                                               (MILL-) MILLENNIUM
                                                                                                                                                                                                                                                                                                                                        20-FEB-2001; 2001WO-US005171.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 GGACGAGTGTGCCGTGTCTCGGGACGGCGGGAGCTCATCTGCTGTGACGGCTGCCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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76; Conserv
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Endege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression marker cDNA 44211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.4%;
                                                               PREDICTIVE MEDICINE INC
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   Monahan JE;
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Pred. No. 0.16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>.
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밁 Ś S

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

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RESULT 70
ABV29094
ID ABV29
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Best Local
                                                                                                                                            17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) assessing the prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 29085
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 539 BP; 125 A; 148 C; 150 G; 115 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                     20-FEB-2001; 2001WO-US005171
                                                                                                                                                                                                                                                                                  23-AUG-2001.
                                                                                                                                                                                                                                                                                                               WO200160860-A2
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV29094 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662795/76
                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 GGGACGGCGGGAGCTCATCTGCTGTGACGGCCTGCCCTCGGGCCTTCCACCTGGCCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCCCCTCCGCTCCGGGAGATCCCCCAGTGGGACCTTGGAGGTGCTCCAGCTGC 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 8783; 11750pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAMACCCTCCCCTGCCTGACATTCCCAATGGTGAATGGCTGTGTCCCCGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                    Endege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%;
                                                                                    Š,
                                                                                    Monahan
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
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Claim 1; Page 6175; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has metastatized in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) assessing the aggressiveness or indolence of prostate cancer in a patient.

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RESULT 71
ADC30621
ID ADC30621
AC ADC30
XX ADC30
XX ADC30
XX Human
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Zhou P,
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                               New polynucleotide and polypeptide useful for diagnosing, preventing of treating conditions such as neurodegenerative diseases, anemias, platedisorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel cDNA sequence,
                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                  Haley-Vicente D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecular weight marker; food supplement; antiparkinsonian; nootropic neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC30621 standard; cDNA; 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ulcers; osteoporosis; autoimmune disease; cancer;
                                                                                                                                                                                                                           2003-371981/35.
                                                                                                                                                                                                                                                                                                                                         Ghosh
                                                                                                                                                                                                                                                                                                                                 Zhang J,
Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                      Drmanac RT;
                                                                                                                                                                                                                                                                                                                                 Ren F,
Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; gene;
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                                                                                                                                                                                                                                                                                                                                     Xue AJ, Zhao
Ma Y, Asundi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
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                                                                                                                                                                                                                                                                                                                                 Wang J,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                         Wehrman
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Contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628 cADC33394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disorders, wounds, burns, ulcers, osteoporosis, autolimune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence expresents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                      Matches
                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 971 novel human cDNA sequences (ADC29919-ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the movel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention, an antibody against a polypeptide of the invention; an entibody applynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of polypuptide of the invention further discloses methods of polypuptide of the methods of and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 control of the control of the invention.
                                                                                                                                                                                                     Sequence 1670 BP; 374 A; 596 C; 488 G; 212 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                            Local
                                                                                                      94;
                                                                                                                                 Similarity
                                ATGAGGACGAGTGTGGCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 703; 1185pp; English
ACGATGAGCACTGTGCCGCCTGCAAGCGAGGGGCCAACCTGCAGCCCTGCGGCACCTGCC
                                                                                                      Conservative
                                                                                                                         3.4%;
                                                                                                   0;
                                                                                                                              Score 52;
Pred. No.
                                                                                                      Mismatches
                                                                                                                                                          띪
                                                                                                                         .18;
                                                                                                                                                       10; Length 1670;
                                                                                                      70;
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                                                                                                   0;
                                                                                                   Gaps
                                                      588
  1142
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GGGACGGCGGGAGCTCATCTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCC

Matches Query Match Best Local :

Similarity

3.4%;

Score 52.2; Pred. No. 0.

B

Length 539; Indels

Conservative

0;

Mismatches 0.14;

38; 5;

0;

612

Sequence 539 BP; 125 A; 148 C; 147 G; 113 T; 0 U; 6 Other;

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110

TANACCCTCCCCTGCCTGACATTCCCAATGGTGAATGGCTGTGTCCCCGATGC TGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGC 665 

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GGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAG
1246
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AAK99602 standard;
MDDT related human
                      10-APR-2003
                     (first entry)
DNA SEQ
                                                                 DNA; 1965
ID No
 66
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Cytostatic; antiatherosclerotic; osteopathic; antianteriosclerotic; hepatotropic; antipsoriatic; antiallergic; antianaemic; antiasthmatic; antityroid; antiinflammatory; anthelmintic; antidiabetic; nephrotropic ophthalmological; immunosuppressive; dermatological; antiulcer; antiparastic; antiarthritic; antibacterial; virucide; funglicide; antiparastic; protozoacide; tranquiliser; vulnerary; anti-HIV; nootropic; neuroprotective; anticonvulsant; cerebroprotective; neuroleptic; molecules disease detection and nephrotropic;

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The invention relates to an isolated polypeptide chosen from molecules CC for disease detection and treatment (MDDT), comprising a one of 39 114-CC 1250 residue amino acid sequences, given in the specification, or a biologically active or immunogenic fragment of the isolated polypeptide. CC effectiveness as an agonist or antagonist of the isolated polypeptide. CC The isolated polypeptide is useful for screening a compound for CC effectiveness as an agonist or antagonist of the isolated polypeptide. CC The isolated polypeptide is also useful as an immunogen for preparing CC polyclonal or monoclonal antibodies by hybridoma technology. The isolated polypeptide and its encoding polynuclectide are useful for diagnosis, CC treatment and prevention of cancer, actinic keratosis, arteriosclerosis, CC atherosclerosis, bursitis, cirrhosis, hepatitis, porriasis, AIDS, adult C asthma, atherosclerosis, osteoporosis, autoimmune haemolytic anaemia, CC autoimmune thyroiditis, Costeoporosis, autoimmune haemolytic anaemia, CC autoimmune thyroiditis, costeoporosis, autoimmune haemolytic anaemia, CC colitis, haemodialysis, uvestis, viral, bacterial, fungal, parasitic, CC protozoal, helminthic infections, trauma, Alzheimer's and Pick disease, CC protozoal, helminthic infections, trauma, Alzheimer's and pick disease, CC extrapyramidal disorder, motor neuron disorder, and other developmental CC metabolic endocrine and rovic monathies mericalar according disorders of the central nervous system, neuromuscular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2001; 2001US-0293723P.
01-JUN-2001; 2001US-0295257P.
08-JUN-2001; 2001US-0297220P.
21-JUN-2001; 2001US-0300526P.
29-JUN-2001; 2001US-0301874P.
22-FEB-2002; 2002US-0359413P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel molecules for disease detection and treatment and polynucleotide encoding them useful for diagnosing, preventing or treating cell proliferative, autoimmune/inflammatory, neurological and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-140448/13.
P-PSDB; AAO26249.
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Zebarjadian Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          periodic paralysis; mental disorder; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260pp; English.
nervous system, neuromuscular disorders, toxic myopathies, periodic paralysis. me
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MG, Yang
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밁
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Best Local (
                      The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention.
                                                                                                                                                                                                             New polynucleotides and developing a diagnostic expression and activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders including mood, anxiety and schizophrenic disorders, anaemia, renal tubular acidosis, epilepsy, hypothyroidism, glaucoma, sensorineural hearing loss and cataract. This polynucleotide sequence represents the DNA encoding a human MDDT protein relating to the invention
                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2002; 2002EP-00008400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1347046-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM02221 standard;
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                                                                                                                                                                                                                                                                                     WPI; 2003-723558/69.
                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2002; 2002JP-00137785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                Yamamoto J, Isono
Beki N, Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                          (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                     SEQ ID NO 906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAGGACGAGTGTGCCGTGTGTCGGGGGGAGCTCATCTGCTGTGACGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGATGAGCACTGTGCCGCCTGCAAGCGAGGGGCCAACCTGCAGCCCTGCGGCACCTGCC
                                                                                                                                                                                                                                                                                                                                            Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                  Isono Y,
ikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention SEQ ID NO: 906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy;
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                                                                                                                                                                                                                                                                                                                Otsuki T, Wakamatsu A,
Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, P
                                                                                                                                                                                                           polypeptides are useful marker or medicines for , or as a target of gene
                                                                                                                                                                                  305pp; English.
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Pred. No.
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Best Local (
                    The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding with the antibody of the encoded protein, and observing the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ss; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related osteoporosis; neurological disease; cancer; tumour.
                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                    New polynucleotides and polypeptides, useful marker or medicines for regulation of their \epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2001; 2001JP-00379298
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  between the two, a transformant carrying the polynucleotide
                                                                                                                                                                                                                                                                                                       as targets of gene therapy.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                                                                                                                                                                                                                                      Page; 222pp; English.
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Yamamoto Seki N,

Yoshikawa

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Otsuki T, Wakamatsu A, Hio Y, Otsuka K, Nagai Otsuka M, Nagahari K, I

Masuho Sato H,

Ishii S;

Tamechika

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Sugiyama T, Isono Y,

[sogai T,

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Matches 94
                                                                                                                                                                                                                                                                                                                                                                       Homo
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25-JAN-2002;
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RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                2001JP-00379298
2002US-00350978
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/product= "Clone FCBBF30142290 protein"
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence presented is a CDNA of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                       Human soft tissue sarcoma-upregulated DNA - SEQ ID 7339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 222pp; English
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                             26-NOV-2003; 2003WO-US038193.
                                                                                                      10-JUN-2004.
                                                                                                                                                                        WO2004048938-A2
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGATGAGCACTGTGCCGCCTGCAAGCGAGGGGCCAACCTGCAGCCCTGCGGCACCTGCC
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57.3%;
                                                                                                                                                                                                                                                                                                                                                     cytostatic;
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Pred. No. 0.21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     gene therapy; vaccine; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                          Plant; bacterial infection; fungal infection; viral infection; rice; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                            Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3710 BP; 784 A; 1129 C; 1032 G; 698 T; 0 U; 67 Other;
                                                                                           22-JUN-2001; 2001WO-IB001105
                                                                                                                                                         22-JUN-2001;
                                                                                                                                                                                                                       03-JAN-2003
                                                                                                                                                                                                                                                                                     WO2003000898-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-2002; 2002US-0429739P
                                   (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGGGCCTACCTCAGCTGCCTGGAGCCGCCCTCAAGACGGCGCCCAAGGGCGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID 5263
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                                                                                                                                                            2001WO-IB001105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; I
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Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                             1194
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Quan
                                                                                                                                                                               GAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTGCC
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CKRSKMSAWSKSMRSSRKCRKCASKRSSAKR
                                           GAGTCCCTTCTGAGCGAGCACACCTTCGATG
                                                                                                                                 CCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTG
                                                                                                                                                                                                                            ACGTGACCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCCCAGC----CCCCGCCCGCCTGGCC
                                                                                                                                                                                                                                                                                                                        ACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCCAGATCCTGCTCAGGAG
                                                                                                                                                                                                                                                                                                                                                                MRWRMWRMTRRRRWAKKSSRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGTGTGGGGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTGCGCGTTGCGGGGTGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSYSWACSSYTWCRSKRRSMMWKMMRKMRWSRSYGWYSWSYKMWMCTAYKKSYYSRWCYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGCCACCCGTGGAGACCCCGCTCCCCCCGGGGCTTAGGTCGGCGGGAGGAGGAGGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCTGCCTGCAGGCAACAGTCCAGGAGGAGGTGCAGCCCCGGCCAGAGGAGGAGGAGCCCCGGCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSAGWKSRCSSWRGRRRMYMAGMMSCARMGSSRMSRKMGSMSKYRKCSSCGKCKMTTRRK
                                                                                      CWYRGKGYYWAGMWMKRYKRMYMYKMWWYKRKYSKCSWYCKMSYYASCMKSARKAGAKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRGGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGMKRGWWAGRMMMRSMCRWSKACYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTGCACCCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKYKS--GSMSKRMWMSSCGRSGCGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRAYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCT-ACAAGCACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 5263; 899pp; English.
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S, Tao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.3%;
10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Zhu
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The present sequence encodes a human nucleic-acid associated protein designated NAAP-31. NAAP sequences have antiparkinsonian, nootropic, neuroprotective, muscular, neuroleptic, antidiabetic, antithyroid, cytostatic, dermatological, antiinflammatory, immunosuppressive, antiallergic, nephrotropic, virucide, antibacterial, fungicide, antiparasitic, protozoacide, antihelminthic, antiarteriosclerotic, cardiovascular, gastrointestinal and hepatotropic activities, and can used in gene therapy. The NAAP polypeptide or its fragments, and the polymucleotide encoding the polypeptide are useful in diagnosing,

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ADJ37277
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30-AUG-2002; 2002US-0407068P.
26-SEP-2002; 2002US-0414139P.
05-NOV-2002; 2002US-0424094P.
17-JAN-2003; 2003US-04240912P.
24-JAN-2003; 2003US-0442419P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic; cardiovascular; gastrointestinal; hepatotropic; gene therapy; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; muscular disorder; myotonic dystrophy; catatonia endocrine disorder; diabetes; Grave's disease; cancer; leukaemia; cervical cancer; breast cancer; immunological disorder; scleroderma; systemic lupus erythematosus; allergy; gastrointestinal disorder; crohn's disease; renal disorder; acherosclerosis; hepatic diseases; cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forsythe IJ, Elliott VS, Le
Khare R, Marquis JP, Becha
Griffin JA, Lee S, Yue H,
Gera M, Gietzen KJ, Nguyen
                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                        New nucleic acid-associated proteins (NAAP) polypeptides, useful diagnosing, preventing and treating disorders with abnormal activ NAAP, e.g. neurological, immunological, cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-2003; 2003WO-US023245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppressive; antiallergic; nephrotropic; virucide;
fungicide; antiparasitic; protozoacide; antihelminthic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan; nucleic-acid associated protein; NAAP-31; NAAP; antiparkinsonian; nootropic; neuroprotective; muscular; neuroleptic; antidiabetic; noithyroid; cytostatic; dermatological; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ37277 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ37242.
                                                                                                                                                                                                                                                                    SEQ
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IJ, Elliott VS, Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "nucleic-acid associated protein NAAP-31"
                                                                                                                                                                                                                                                                 66;
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                                                                                                                                                                                                                                                                 290pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang:
S, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang
DB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X, Jackson AA, Kable AE, SY, Lee EA, Ison CH, Ha. DD, Bulloch SA, Blake JJ, ang YG, Sprague WW, Baugh B, Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baughn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE, Tang YT;
Hafalia AJA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial;
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RESULT 79
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Best Local S
Matches 71
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                                                                                                                                                                                                                              length cDN
diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequence SEQ ID NO:15067.
The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises
(a) an oligo-dT primer and an oligonucleotide complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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27-AUG-1999;
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                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                       Ś
                                                                                                                                   8
                                                                                                                                                                                                                sets for synthesizing polynucleotides, particularly the 5602 full-
. CDNAs defined in the specification, and for the detection and/or sets of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer;
                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsu
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                                                                                                                                   SEQ
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99JP-00300253.
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                                                                                                                         15067; 2537pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashi K,
A, Nagai K,
                                                                                                                            Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                       Saito K,
C, Otauki
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                              comprises:
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Matches 71
                                                                                                             19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                              03-FEB-2000;
27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and an oligonuclectide comprising a sequence complementary to a polynuclectide which comprises a 3'-end sequence, where the oligonuclectide which comprises at least 15 nuclectides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13632 to AAH19742 represent human cDNA sequences; AAB2246 to AAB95893 represent human amino acid sequences; and AAH13622 to AAH13632 represent coligonuclectides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
             Tang YT, Liu C, Ma Y, Zhao QA, Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                  WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK52998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3079 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 65.771; Conservative
                                                                               HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                               system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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2000US-00560875
2000US-00598075
2000US-00620325
2000US-00620325
2000US-00654936
2000US-00693325
2000US-00693325
2000US-00728422
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             Wang D, W
, Wejhrman
                           Drmanac RT,
Wang D, Wang
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65.7%;
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Pred. No. 0.
               Asundi V,
JJ, Zhang
Goodrich R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .97;
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                                                Zhou P,
                                Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
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                                Chen
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                               Wang ZW;
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RESULT 81
AAK52014
ID AAK52
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Best Local Similarity
Matches 108; Conserv
03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM7823-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiations. The production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis, tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 4806-4807; 6221pp; English.
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                       Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                               05-FEB-2001;
                                                                                                                               09-AUG-2001
                                                                                                                                                            WO200157190-A2
                                                                                                                                                                                                                        nervous system
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                                                                                                                                                                                                                                                                                                       polynucleotide SEQ ID
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                  2000US-00560875.
2000US-00598075.
2000US-00620325.
                                                                2000US-00496914.
                                                                                               2001WO-US004098
                                                                                                                                                                                                                         disorder;
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                                                                                                                                                                                                                         arthritis;
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                                                                                                                                                                                                                                                                      gene therapy;
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Best Local S
Matches 108
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Ma Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2179
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20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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P-PSDB; AAM78881.
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/, Zhao QA, 1
AJ, Yang Y,
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271
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                                                                                                                                                                           TGCCTGCAGGACACTCCAGGAGGTGCAGCCCCGGCAGAGGAGGAGCCCCGGCCCAGGAG
                                                                                                                                                                                                                                           GCCGCCCGCCAGCTCAAGCGCAGCCACGTGCTCCCCCGAGGGCCGCTCGCCCGGGCCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                          GCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCCGGGCCTTCCAC
                                                         CCACCCGTGGAGACCCCGCTCCCCCCG 749
                                                                                                                     GCCCTTAÁGCACCCGGCCACCAÁGGACCTGGCGGCÁGCCGCACACGGGCCCCÁGCTG
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   CCGCCCCCGCAGGCCCAGCCCAGCCG
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Wejhrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 A; 757 C; 689 G; 375 T; 0 U; 0 Other;
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lang D, Wang
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Pred. No. 1;
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J, Zhang
Goodrich R
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   297
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RESULT 82
ADO35478/c
ID ADO35
viral
                                                       mouse; murine; cancer; psoriasis; ulcerative colitis;
ischaemic heart disease; thrombosis; immune disorder;
        WO2004046310-A2
                          Mus sp.
                                                                                 Novel mouse
                                                                                                    26-AUG-2004
                                                                                                                                        ADO35478 standard;
                                                      schaemic heart
                                                                                                                                                  ò
                                             disorder;
                                                                                 gene sequence
                                                                                                  (first entry
                                            disease; thrombosis; immune
ds; gene.
                                                                                                                                        DNA;
                                                                                 #151.
                                                       inflammation;
bacterial disorder;
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RESULT 83
AAS75442
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Best Local Sim
Matches 135;
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05-DEC-2002;
05-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                   Sequence 3005 BP; 782 A; 632 C; 849 G; 742 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                      The invention comprises 744 novel mouse DNA sequences (genes). The DNA sequences of the invention are useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischaemic heart disease, thrombosis, immune disorders, bacterial disorders and viral disorders. The present nucleic acid represents a mouse DNA sequence of the invention. NOTE: The present DNA sequence is not shown in the specification, but has been retrieved from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mouse nucleic acid molecules and polypeptides, useful for treating cancer, psoriasis, ulcerative colitis, inflammation, ischemic heart disease or thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams LT,
                  DNA encoding novel human diagnostic protein #11246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 151; 263pp; English.
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-2003;
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                                      13-FEB-2002
                                                                          AAS75442 standard;
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                                                                                                                                                                                                                                       GCTGGGTGACGAAAGCTCTCCCGCTGGCGGCCCCGGACGCTCCTCTAAGCCGAGCCCGGCA
                                                                                                                                                                                                                                                                           GAGCCGCCATGTCGGTGCGCCCACCCGTCGCTGCGGCTCGGGGCCCGGTCGCCGGC
                                                                                                                        CCTCGCGCGTCTGGGAGCTCGCCGTGTCCCCCTCAGCCCAG
                                                                                                                                        caregocogrocescococorrococos
                                                                                                                                                             2002US-0431445P
2002US-0471662P
2003US-047662P
2003US-0476632P
2003US-0485217P
2003US-0485217P
2003US-0493335P
2003US-0493332P
                                                                                                                                                                                                                                                                                                                Conservative
                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIME THERAPEUTICS
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                                                                          CDNA;
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Pred. No. 1.4;
D; Mismatches 145;
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RESULT 84
AAH33830
ID AAH33
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AC AAH33
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DT 03-SE
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DE Humar
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cc reaction (PCR) primers, oligomers, and for chromosome and gene mapping, cand in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cc genes. (I) is useful in gene therapy techniques to restore normal cc useful for generating antibodies against it, detecting or quantitating a cc useful for generating antibodies against it, detecting or quantitating a cc polypeptide in tissue, as molecular weight markers and as a food cc supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The college of the polypucleotide sequences have applications in convolving aberrant protein empping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cc coding sequences of the invention. Note: The sequence data for this cateronic format directly from WIPO at clectronic format directly from WIPO at
                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to assebiodiversity.
                                                                                                                                                                                                                                                                                                                                                             Sequence 924 BP; 259 A; 192 C; 264 G; 209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 11246; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-639362/73
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                                                                                                                                                                             524 GAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYSEQ INC.
                                                                                                                                                                                                                                                                          Similarity
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TTGTTCAAGAGTCTTCCATGAGGACTGCCACATCCCACC
                                                                                                                   GAGAAACTTGGATGAGTGTGAGGTGTGCCGGGACGGAGGGGAGCTGTTCTGTTGCGACAC
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                             3.1%;
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                                                                                                                                                                                                                                      0,
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                Length 924;
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                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                          Gaps
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Human colon cancer antigen encoding cDNA SEQ ID NO:886.

AAH33830; 03-SEP-2001

(first entry)

AAH33830 standard;

CDNA; 1006

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RESULT 85
AAH16455
ID AAH16
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AC AAH16
XX
DT 26-JU
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200122920-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; colon cancer; colon cancer antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1006 BP; 339 A; 191 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000; 2000WO-US026524.
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                 26-JUN-2001
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                                               AAH16455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                              AAH16455 standard;
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                                                                                                                                                                                               648
                                                                                                                                                                                                                              293
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                                                                                                                                                                                                                                                                                               233
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                                                                                                                                                                                                                                                    CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCC
                                                                                                                                                                                                                                                                                                                        AATGAGGACGAGTGTGCCGTGTTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                                                                                               AATGAAGACTGGTGTGTCTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGT
                                                                                                                                                                                             TGGAGGTGCTC 658
                                                                                                                                                                                                                                CCAAAGGTCTTTCATCTAACTTGTCATGTTCCAACACTACTTAGCTTTCCAAGTGGGGAC
                                                                                                                                                               TGGATATGCAC
                                                                                                                                                                                                                                                                                                                                                              Conservative
               (first entry)
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99US-0163280P
                                                                              cDNA;
                                                                                                                                                                                                                                                                                                                                                                            3.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
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diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birse CE,
                                                                              2724
                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                            Score 47.8;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cancer-associated polypeptides,
and/or treating colorectal cancers.
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                                                                                                                                                                                                                                                                                                                                                            52;
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                                                                                                                                                                                                                                                                                                                                                                  cc uncleotide sequences defined in the specification, where the complementary strain of a polynucleotide; or (b) a combination (c) of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination (c) of an oligonucleotide comprising a sequence complementary to the (c) sequence and an oligonucleotide which comprises a 5'-end (c) sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a complementary to a polynucleotide which comprises a 1'-end sequence, where the combination of comprises at least 15 nucleotides and the combination of coligonucleotide comprises at least 15 nucleotides and the combination of comprises at least 15 nucleotides and the combination of comprises at least 15 nucleotides and the combination of comprises at least 15 nucleotides and the combination of comprises are useful for synthesising polynucleotides, comprises are useful for synthesising polynucleotides, comprises are also useful for the comprise of the full-length cDNAs. The primers are also useful for the comprise of the full-length cDNAs. The primers are also useful for the comprise of the full-length cDNAs. The primers also useful for the comprise of the full-length cDNAs. The primers also useful for the comprise of the full-length cDNAs. The primers also useful for the comprise of the sequences; and AAH1362 to AAH13628 and comprise of the 
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Matches 79
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Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for a length cDNAs defined in the specification. Where
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2000;
02-MAY-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA sequence SEQ ID NO:15457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000;
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                                                                                                                                   1953
                                               2013
    648
                                                                                                                                                                          528 AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
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                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                       invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
    TGGAGGTGCTC
                                               CCAAAGGTCTTTCATCTAACTTGTCATGTTCCAACACTACTTAGCTTTCCAAGTGGGGAC
                                                                                      ccregeccrrccaccreeccreccreccreccreecreecreesaarccceaereece
                                                                                                                                   AATGAAGACTGGTGTGTCTGCCAAAACGGAGAGATCTCTTGTGCTGCGAAAAATGT
                                                                                                                                                                                                                                                                                                            2724 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO 15457; 2537pp +
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1 T, Wakama
                                                                                                                                                                                                                                          3.1%;
    658
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Wakamatsu
                                                                                                                                                                                                                                                                                                              602
                                                                                                                                                                                                                     Score 47.8; DB Pred. No. 1.6; 0; Mismatches
                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                            C; 590 G;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                            627 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for synthesising 5602 full-
where a primer set comprises:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listing; English
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C, Otsuki
                                                                                                                                                                                                                          52;
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                                                                                                                                                                                                                                                                Length 2724;
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                                                    2072
                                                                                                                                        2012
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TGGATATGCAC 2083

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RESULT 86
ADP13566
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                                                                                                                                           The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having conn-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes of the genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample comprises enriched PBMCs. The peripheral blood sample is a whole blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples tislated at different stages of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a gene that differentially expressed and detected by the method of the invention. (Note: this sequence is not given as part of the printed specification but was obtained from WIPO in electronic format at
                                                           Query Match
Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes
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Sloni
                                                                                                                      Sequence 3424 BP; 1029 A; 811 C; 843 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2002; 2002US-0427982P.
03-APR-2003; 2003US-0459782P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004048933-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP13566 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2003; 2003WO-US037481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Renal cell carcinoma differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TWIN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DORN/)
2669
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) TREPICCHIO W
) DORNER A.
) STOVER J A.
) SLONI D K.
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                                                                        Similarity
AATGAAGACTGGTGTGTGTGTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGT
                          AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burczynski
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 302; 350pp; English
                                                           Conservative
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                                                       Score 47.8; D
Pred. No. 1.6;
O; Mismatches
                                                                                                                      741 T; 0 U; 0 Other;
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2740 AATGAAGACTGGTGTGTCTGCCAAAACGGAGAGATCTCTTGTGCTGCGAAAAATGT

2799 647

587

AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGC

588 CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACC

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RESULT 87
ADB80996
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  Query Match
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Matches 79
                                                                                                                                                              The invention relates to a novel isolated protein complex comprising a RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a Gag late domain, PI3K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A, STAM2B, VHS-UIM, a GTP8se, an E2 enzyme, tsg101, a cullin, RING-SH, and a clathrin. The novel protein complex has virucide activity and can be used to treat disorders as part of a vaccine. The protein complex and composition are useful for detecting cells infected with a virus, for dentifying agents having antiviral activity, and for treating viral disorders caused by retroviruses, rhabdoviruses, or filoviruses. This polymucleotide represents a DNA sequence relating to a protein comprising the RING-SH complex of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated protein complex comprising a RING-SH 3 polypeptide and another polypeptide, useful for detecting cells infected with a virus, and for treating viral disorders caused by retroviruses, rhabdoviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RING-SH 3; Gag protein; Gag late domain; PI3K; actin; myosin; Hsp60; Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tegcullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 69; 176pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2001; 2001US-0308958P
09-NOV-2001; 2001US-0345846P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RING-SH complex related DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2002; 2002WO-US024589
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                                                                                                                    BP;
                                                                                                                 1044 A; 832 C;
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                                                                                                                 886 G;
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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated disease detection and treatment (MDDT) DNA polynucleotide. The polynucleotide of the invention demonstrates antiarteriosclerotic, antipsoriatic and cytostatic activities and may be useful in a composition for detecting the expression of a disease detection and treatment molecule polynucleotide. The molecules of the invention may be utilised to diagnose or treat conditions, diseases or disorders associated with cell signalling, such as arteriosclerosis, psoriasis and cancer. The current sequence is that of a human MDDT cDNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones AL, Dahl CR, Gietzen D, Chinn J, Dufour GE, Jackson JL,
Yu JY, Tuason O, Yap PE, Amshey SR, Dam TC, Liu TF, Gerstin
Peralta CH, Lewis SA, Chen AJ, Marwaha R, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease detection; MDDT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2002; 2002US-0349413P
17-JAN-2002; 2002US-0349946P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-2003; 2003WO-US001363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arteriosclerosis, psoriasis, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated disease detection and treatment diagnosing or treating conditions associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ADL22668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 13; 411pp;
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                                                       CCAAAGGTCTTTCATCTAACTTGTCATGTTCCAACACTACTTAGCTTTCCAAGTGGGGAC
                                                                                                                                                                   AATGAAGACTGGTGTGTCTGCCAAAACGGAGGAGATCTCTTGTGCTGCGAAAAATGT
                                                                                                                                                                                                                                                                                                                                                                                           6730 BP; 2123 A; 1184 C; 1206 G;
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sclerosis; psoriasis; cancer; human; ss; gene
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Matches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIG16176-ABIG30511), expressed DNA sequences (ABIG16176-ABIG30511), expressed DNA sequences (ABIG16176). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direct from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 14747; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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  382
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                                                                                                                                                                                                                                                                                                                                                                            AGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCT 585
                                                                                                           GTGGCCAGTGGCTGTGCCACAGCTGTCGCATGAGCAAGCTCTCCCAGCCGCCGGCCTCCT 381
                                                                                                                                                                                                                                                                                                                                         CATCCAAGGCCAGTTCCGTGGAGC
                                                    CAGAGGAGCCCCGGCCCCAGGAGC
                                                                                                                                                                GTGGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGG
                                                                                                                                                                                                                          GCCCCTCCAGCTTCCACCTGCAATGCCATGATCCACCGTTGAGCGAGGAGGACATACCCA
                                                                                                                                                                                                                                                                GCCCTCGGGCCTTCCACCTGGCCTGCCTGCCTCCGCTCCGGGAG-----ATCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%;
ilarity 55.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              793 A; 935 C; 890 G; 605 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 3223
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Pred. No. 1.8;
0; Mismatches
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RESULT 91
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AAV24559
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Matches
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                        This sequence encodes the leukocyte specific protein, Sp140 of the invention. The Sp140 polypeptides act as gene transcription regulators. They can be used to develop products for use in the diagnosis and treatment of autoimmune diseases such as primary bilary cirrhosis, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, scleroderma and multiple sclerosis, viral diseases including those caused by herpes simplex virus, cytomegalovirus, HIV, hepatitis virus, human T-cell leukaemia, virus-1 (HTMV-1) and adenovirus, and cancers including leukaemias, particularly acute promyelocytic leukaemia, cancers of the breast, ovary, prostate, bone, liver, pancreas or spleen, sarcomas and
                                                                                                                                                                                                                  Sequence 2905 BP; 874 A; 610 C; 760 G; 661 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 54-57; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated gene transcription regulator, Sp140 - used to develop products for the diagnosis and treatment of auto-immune diseases, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-286419/25.
P-PSDB; AAW57747.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leukocyte specific protein, Sp140,
                                                                                                                                                                                                                                                                                                                                                                                                                                         infections or cancers.
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(вгос/) вгосн
                                                                                                                                                                             Local
                                                      1876
                                                                                                                                                                             Similarity
                                                                                                                        CCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTG
                                                                                                          CCCTTGTATGAGAAACCTGGATGAGTGTGAGGTGTGCCGGGACGGAGGGGAGCTGTTCTG
                                                      TTGCGACACTTGTTCAAGAGTCTTCCATGAGGACTGTCACATCCCGCC
                                                                              crereacecrecerceeeccrrecaccreeccreccrereccrec
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                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product="Sp140"
                                                                                                                                                                            64.8%;
                                                                                                                                                                                         3.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; gene transcription regulator; therapy;
infection; cancer; ds.
                                                                                                                                                               0,
                                                                                                                                                                            Score 47.2;
Pred. No. 2.
                                                                                                                                                               Mismatches
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                                                                                                                                                                                          멂
                                                                                                                                                               38;
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                                                                                                             Best Loc
Matches
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                 Sequence 2911 BP; 878 A; 609 C; 759 G; 665 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 11248; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic d
                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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23-AUG-2000;
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                                                                                                                            Local
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                                                                                                                                Similarity
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                                                                CCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTG
 CCCTTGTATGAGAAACCTGGATGAGTGTGAGGTGTGCCGGGACGGAGGGGAGCTGTTCTG
                                                                                                           3.1%;
ilarity 64.8%;
Conservative (
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2000US-00649167
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                                                                                                           Score 47.2; DB
Pred. No. 2.1;
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1876 TTGCGACACTTGTTCAAGAGTCTTCCATGAGGACTGTCACATCCCGCC 1923

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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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upplement; medical imaging; diagnostic; genetic disorder; ss
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TTGCGACACTTGTTCAAGAGTCTTCCATGAGGACTGTCACATCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             987
                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 47.2; DB Pred. No. 2.1; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        866 G; 721 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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2275
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584 CTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCC-----GCTCCGGGAGATCC

647 636

GAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGGGGAGCTCATCTGCTGTGACGG 583

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Matches 106;
                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                       reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and and and and and are applied to assess biodiversity and and and and are applied to assess biodiversity and partners are useful for the polynucleotide sequences have application of mutations to responsible for genetic disorders or other traits to assess biodiversity and partners are useful for the polynucleotide sequences have application of mutations are separated to assess biodiversity and partners are useful for the polynucleotide sequences have application of mutations are separated to a page and pa
                                                                                                                                                          and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 11249; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                            Sequence 1210 BP; 248 A; 321 C; 368 G; 273 T; 0 U; 0 Other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABG11258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #11249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-)
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  Conservative
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                            3.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as hybridisation probes, polymerase
  0;
                               Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽P
Mismatches
                                                         DB
                                                         5
  70;
                                                      Length 1210,
     Indels
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  7;
     Gaps
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708 697 768 768 768 768 768 768 768 768 768 76	648 TT
	TIGTTCAAGAGTCTTCCATGAGGACTGCCTGCAGGAGGTAGAAGAGTGCAGCCCC
GCGCACTCTCCAGCAG	  CATGAGGACTGT
GAGTGCCGGCTTG	 
TTGTGTCTAGATGGGGAA  cine motility polyp  uterus; pregnancy;	  GTGGAAGCTGAC
. c o	 BAGGGATCT 707
	<del></del>
***************************************	PR RG RG RG RG RG RG RG RG RG RG RG RG RG
08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 25-SEP-2000 25-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 20-OCT-2000 20-OCT	
01 2000US. 01 2000US. 02 2000US. 03 2000US. 04 2000US. 05 2000US. 06 2000US. 07 2000US. 08 2000US. 09 2000US.	
0.0231240 0.0231244 0.0231244 0.023210814 0.023221814 0.023221814 0.023221814 0.023221814 0.023221814 0.023221814 0.023221814 0.02322181 0.02322181 0.02322181 0.02322181 0.02322181 0.02322181 0.0232221 0.0232221 0.0232221 0.0232221 0.0232221 0.0232221 0.0232221 0.0232221 0.0232221 0.02322221 0.02322221 0.0232222222222222222222222222222222222	022295

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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Best Local Similarity
                                                                                                                                                                                                                                                                                              Matches 143;
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11-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
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11-DEC-2000
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11-DEC-2000
11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of novel human uterine motility-association polypeptides (AAU18094-AAU1812), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAS28995-AAS29020 represent genomic sequences encoding for novel human uterine motility-association polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                       Sequence 6610 BP; 1208 A; 2130 C; 2123 G; 1149 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing, pused as food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                          1186
                                                                                   1126
                                                                                                                                               1066
                                                                                                                                                                                                          1006
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243
                                                                                                                 127
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                                                                                                                                                                                                        ACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGAT
                                                                                                                                                                                                                                                                  GCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCCGCTGCCTTCC
                          ATGACCTGGAGTCCCTTCTGAGCGAGC 1212
                                                                               gccrggcccrggggcrgccAAggArgAcAcrgccAgrcAcGAGcccgcrcrgcAcAgag
                                                                                                                                                                            GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGT
                                                                                                                                                                                                                                    GCTGTCAGTGCCGCGAGCGTACGTTCGGCGCGCGCGCTGCGATCGCTACTGCCAGTGCTTCC
GTGAGGCGGGTCCCAGCCTTCCCTAGC
                                                      ĠĊĠĊĠĠŦĊŦĊŤĊĠĠĊĊAĠĠĠĀĠĠĀĠĠĀĠĠĀĠĠŦĠĠAAĠĠĠĊĠĠĠĊĊĠĊĊĠAŦĠĠĠĠĀĊĀĠĠĠ
                                                                                                                 ACTG-TCGCGAGCCGTGCCCCGGCCGGCTTCTACGGCTTGGGCTGTCGCCG---CCGGTAA
                                                                                                                                               CCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGTGCTGGCCCCCAGCCCCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0249216P
2000US-0249211P
2000US-0249214P
2000US-0249244P
2000US-0249265P
2000US-0249265P
2000US-0249265P
2000US-0249297P
2000US-0249290P
2000US-0249290P
2000US-0251910P
2000US-0251930P
2000US-0251931P
2000US-0251868P
2000US-0251868P
2000US-0251869P
2000US-0251990P
2000US-0251990P
2000US-0251990P
2000US-0251990P
2000US-0251990P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 148; 524pp; English.
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                             3.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM;
                                                                                                                                                                                                                                                                                                             2.6;
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                                                                                   1185
                                                                                                                                               1125
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RESULT 95
AAS29013
ID AAS299
XX AAS29
X
                     14-AUG-2000
12-AUG-2000
22-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
21-SEP-2000
01-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence #19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2001
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2000US-0190076

2000US-0205515p

2000US-0205515p

2000US-0215135p

2000US-021647p

2000US-021647p

2000US-0217486p

2000US-0217487p

2000US-022964p

2000US-0225214p

2000US-0225214p

2000US-0225214p

2000US-0225214p

2000US-0225268p

2000US-0225268p

2000US-0225758p

2000US-0225759p

2000US-0227182p

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human uterine motility polypeptide.
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RESULT 96
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ID AAS26
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Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of novel human uterine motility-association polypeptides (AAU18094-AAU18152), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polymucleotide sequences of the invention are also useful in gene therapy. AAS28995-AAS29020 represent genomic sequences encoding for novel human uterine motility-association polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
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             07-NOV-2001
                                           AAS26967;
                                                                    AAS26967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6610 BP; 1208 A; 2130 C; 2123 G; 1149 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosing, preventing, treating or amelused as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 147; 524pp; English.
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                                                                                                                                                                     ATGACCTGGAGTCCCTTCTGAGCGAGC 1212
                                                                                                                                                                                                                                                                                                                                                                                           GCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGTGTGCGTTACTCACTGCGCCGCTGCCCTTCC
                                                                      standard;
                                                                                                                                           GTGAGGCGGGTCCCAGCCTTCCCTAGC
                                                                                                                                                                                                GCGCGGTCTCTCGGCCAGGGAGGGAGGAGGTGGAAGGGCCGGCGGGCCGATGGGGACAGGG
                                                                                                                                                                                                                           GCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGG 1185
                                                                                                                                                                                                                                                                                                                 GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGT
                                                                                                                                                                                                                                                                                                                                                                         GCTGTCAGTGCCGCGAGCGTACGTTCGGCGCGCGCGCTGCGATCGCTACTGCCAGTGCTTCC
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2000US-0250391P
2000US-0251030P
2000US-0251988P
2000US-025179P
2000US-0251479P
2000US-0251866P
2000US-0251868P
2000US-0251869P
2000US-0251869P
2000US-0251969P
2000US-0251969P
2000US-0251969P
2000US-0259678P
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
             (first entry)
                                                                                                                                                                                                                                                           -TCGCGAGCCGTGCCCCGCCGGCTTCTACGGCTTGGGCTGTCGCCG--
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                                                                      DNA;
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Pred. No. 2.6;
0; Mismatches
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20-OCT-2000
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2000US-023198P 2000US-023198P 2000US-0232398P 2000US-02332401P 2000US-0233063P 2000US-0233063P 2000US-0233499P 2000US-02342749 2000US-02342749 2000US-0235834P 2000US-0235834P 2000US-0235834P 2000US-0235834P 2000US-0235834P 2000US-0235834P 2000US-0236327P 2000US-0236327P 2000US-0236327P 2000US-023637P 2000US-024677P 2000US-0249217P 2

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11-JUL-2000

14-JUL-2000

26-JUL-2000

14-AUG-2000

12-AUG-2000

22-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

20-SEP-2000

01-SEP-2000

01-SEP-2000
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04-FEB-2000

24-FEB-2000

12-MAR-2000

16-MAR-2000

17-MAR-2000

19-MAY-2000

07-JUN-2000

28-JUN-2000

07-JUL-2000

07-JUL-2000

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11-JUL-2000
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-MAR-2000;
-APR-2000;
-MAY-2000;
-JUN-2000;
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 2000US-018464P.
2000US-0189874P.
2000US-0199076P.
2000US-0205159P.
2000US-0215135P.
2000US-021647P.
2000US-021648P.
2000US-021748BP.
2000US-021748P.
2000US-021748P.
2000US-0224518P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
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2000US-0225214P.
2000US-0225214P.
2000US-0225275P.
2000US-0225275P.
2000US-0225759P.
2000US-0225759P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq ID
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14-SEP-2000
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27-SEP-2000
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29-SEP-2000
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29-SEP-2000
29-SEP-2000
20-CCT-2000
21-NOV-2000
21-NOV-2000
20-CCT-2000
20-CCT-2000
21-NOV-2000
2000US-0232398P

2000US-023239P

2000US-0233240P

2000US-02332499P

2000US-023429P

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2000US-023434P

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2000US-023537P

2000US-023637P

2000US-0249937P

2000US-0241787P

2000US-0241787P

2000US-024617P

2000US-024647P

2000US-024647P

2000US-024647P

2000US-02467P

2000US-024921P

2000US-024921P
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The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to grevent, treat or ameliorate a medical condition in e.g. humans, mice, CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC pathological pathological condition or susceptibility to a condition. Antibodies to the proteins can also used in CC pathological condition. Antibodies to the proteins can also be used in CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are disgnosed or treated include autoimmune (CC immunoassays c.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, CC nervous system disorders e.g. alzheimer's disease, infections caused by acteria, viruses and fungi and ocular disorders e.g. corneal infection, CC and many other disorders listed in the specification. The polypeptides CC can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before CC responsation, for supporting cell culture of primary tissues, to responsitive or preservative to increase or decrease storage CC capabilities, fat content, lipid, protein, carbohydrate, vitamins, candidative or preservative to increase or decrease storage CC capabilities, fat content, lipid, protein, carbohydrate, vitamins, cc squence is a genomic DNA encoding a partial novel secreted protein of the invention. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
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05-DEC-2000; 2000US-025119P.
06-DEC-2000; 2000US-0251179P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254997P.
11-DEC-2000; 2000US-0254997P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 303; 601pp; English
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mes 143; Conservative
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                                                                                                                                                                                                                                                                                          GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGTCAGTGCCGCGAGCGTACGTTCGGCGCGCGCGCTGCGATCGCTACTGCCAGTGCTTCC
                                  GTGAGGCGGGTCCCAGCCTTCCCTAGC
                                                                                        ATGACCTGGAGTCCCTTCTGAGCGAGC 1212
                                                                                                                                                                                 GCCTGGCCCTGGGCCAAGGATGACACTGCCAGTCACGAGGCCCGCTCTGCACAGGG
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                                                                                                                                            Barash
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53.6%;
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Pred. No. 2.6;
0; Mismatches 120;
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     ARSSULT 97
ARS261
XX AAS261
XX AAS26
30-JUN-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
26-JUL-2000
14-JUL-2000
14-AUG-2000
15-SEP-2000
01-SEP-2000
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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28-JUN-2000;
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  2000US-0186350P

2000US-0199076P

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2000US-0199076P

2000US-0209467P

2000US-021643P

2000US-0216496P

2000US-0216880P

2000US-0218290P

2000US-0218290P

2000US-0224519P

2000US-0225214P

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2000US-0225214P

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2000US-0225758P

2000US-0225758P
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2000US-0179065P 2000US-0180628P 2001WO-US001320

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Human; immunosuppressive; antiarthritic; ds; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; cardiocaric system disorder; cerebral ischaemia; angiogenesis; nervous system disorder; higherial selass; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; wound healing; epithelial cell proliferation; skin ageing; food additive;
preservative;
                                                                                                                                                                                                                                                                                                                                                                                Human genomic DNA
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antiproliferative.
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08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0231242P. 2000US-0231243P. 2000US-02312449P. 2000US-0231413P. 2000US-0231413P. 2000US-0232080P. 2000US-0232081P.

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                                                                                                                                                                                                                                                                                                                          The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to grevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They are also used to in diagnosing a pathological condition or susceptibility to a condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in claeviating symptoms associated with the disorders and in diagnostic mimunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune cd diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac carrest, cerebrovascular disorders e.g. crecbral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, cand many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, cornearse tsissues and in chemotaxis. The polypeptides can also be used to and in chemotaxis. The polypeptides can also be used cornean, in and in chemotaxis. The polypeptides content, lipid, protein, carbohydrate, tressest to capabilities, fat content, lipid, protein, carbohydrate, The present content, lipid, protein, carbohydrate, by riamins, contents, cornean, contents, and other nutritional components. The present
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the invention:
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ACTG-TCGCGAGCCGTGCCCCGCCGGCTTCTACGGCTTGGGCTGTCGCCG---CCGGTAA
                                                                  GCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGAAGT
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nilarity 53.6%;
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sequence data for this pat
                                                                                                                                                                                                         ; Score 47; DB 4; Pred. No. 2.6; 0; Mismatches
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ADBA06837 standard; DNA; 6610 BP.  ABA06837;  10-JAN-2002 (first entry)  Human genomic DNA SEQ ID NO: 923.  Human; gene therapy; neural disorder; immune system disorder; muscular disorder; cardiovascular disorder; proliferative disorder; reproductive disorder; reproductive disorder; reproductive disorder; proliferative disorder; inflammation; ds.  Hcmo sepiens.  H	1126 GCCTGGCCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGG
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11-DBC-2000;
                                                      Immunostimulant; antirheumatic; antiarthritic; neuroprotective; antiallergic; antidabetic; antiasthmatic; antiinflammatory; nootropic; immunosuppressive; anticoagulant; thrombolytic; antiatherosclerotic; cytostatic; nephrotropic; antiparkinsonian; gynecological; virucide; antibacterial; antiarrhythmic; fungicide; HCFATO5; HWAAB95; HTNBM01; immunodeficiency; autoimmune disorder; allergic reaction; cardiovascularimmunodeficiency; autoimmune disorder; allergic reaction; cardiovascularimmune disorder; allergic reaction; cardiovasc
inflammatory oblood-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides human cDNAs, proteins and related gen DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence of the present s
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Novel polypeptide useful for diagnosis, prognosis, prevention, treatment of immune, hyperproliferative, renal, respiratory,
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BARASH
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CC neurological disorders, endocrine disorders, respiratory disorders. The content of the invention is useful to stimulate neuronal growth and to treat, prevent, and/or diagnose neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions, for stimulating characteristics such as body height, weight, hair color, and to increase or decrease storage capabilities, fat content, lipid, protein, components. The nucleic acid of the invention can be used in gene therapy. This polynucleotide sequence represents one of the novel nucleic acids of the invention
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Matches 143; Conserv
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Patent No. 6329517

GENERAL INFORMATION:

APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred

TITLE OF INVENTION: DERNATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
FILE REFERENCE: 8484-0030-999

CURRENT APPLICATION NUMBER: US/08/913,832A

CURRENT FILING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: PCT/DE96/00444

PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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US-08-254-357-3
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APPLICANT: Seelig, Hans Peter
APPLICANT: Renz, Manfred
TITLE OF INVENTION: DERMATOMYOSITIS-SPECIFIC AUTO-ANTIGEN
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Matches 96; Conserv
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SOFTWARE: FastSEQ fo:
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1996-03-08 NUMBER OF SEQ ID NOS: 2
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CURRENT APPLICATION NUMBER: US/09/158,707
                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE:
                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: (1)...(5736)
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1109 AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGATACCTGTCCCC 1168
                        532 AGGACGAGTGTGTGTGTGGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
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Pred. No. 3.2e-05;
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NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 325
LENGTH: 6475
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
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APPLICANT: Tang, Y.
                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                Query Match
Best Local Similarity
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APPLICANT:
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1447
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                                                                                                                                 1327 AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
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                                                                                              592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCAGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                    532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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Zhang, Jie
Ren, Felyan
Chen, Rui-hong
Chao, Qing A.
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GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG 1482
                             GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
                                                                  GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Zhou, Ping
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di, Vinod
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                                                                                                                                                                                                  Score 60; DB 4;
Pred. No. 3.3e-05;
0; Mismatches 60
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                                                                                                                                                                                                                                  Length 6475;
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                                                                  1446
                                                                                                   651
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RESULT 5 US-07-945-295-1

Sequence 1, Application US/07945295 Patent No. 6610823 GENERAL INFORMATION:

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RESULT 6
PCT-US91-06418-2
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Sequence 2, Application PC/TUS9106418
GENERAL INFORMATION:
APPLICANT: Oklahoma Medical Research, Foundation, et al
TITLE OF INVENTION: Antigens Associated with Polymyositis
TITLE OF INVENTION: and with Dermatomyositis
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Kilpatrick & Cody
STREET: 100 Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1053 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/
FILING DATE: 19920909
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PABST, PATTER L.
REGISTRATION NUMBER: 31,28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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  LIBRARY: Human thymocyte lambda gtl1
  CLONE: L1
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REFERENCE/DOCKET NUMBER: OWRF 120CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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CITY: Atlanta
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                                                                                                                                                                                                                                                                                                        652 GGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGCAGCCCCCGGGCAGAGAG 706
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ilarity 58.9%;
Conservative
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E: Blood
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US-09-976-594-1064/c
; Sequence 1064, Application US/09976594
; Patent No. 6673549
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                                                                               ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORWATION: Incyte ID No.
US-09-976-594-1064
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SEQ ID NO 1064
LENGTH: 2327
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Best Local Similarity
Matches 70; Conserv
  Query Match
Best Local Similarity 50.
Matches 107; Conservative
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APPLICANT: FURINESS, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-10-12 PRIOR APPLICATION NUMBER: 60/240,409 PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1143
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                TYPE: DNA
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PRIOR APPLICATION UNTA:
APPLICATION UNMBER: US 60/027,347
FILING DATE: 02-OCT-1996
CLASSIFICATION: 514
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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REFERENCE/DOCKET NUMBER: 0609.4330001/JAG/BJD
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REGISTRATION NUMBER: 29,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 02-00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1816 CCCTTGTATGAGAAACCTGGATGAGTGTGAGGTGTGCCGGGACGGAGGGGAGCTGTTCTG 1875
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                      2.9%;
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Score 44.6; DB 4; Length 2327; Pred. No. 0.15; O; Mismatches 104; Indels 0
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                                                                                                                                                       ; LOCATION: US-08-340-203A-1
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                                                                                           Matches 107;
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                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MOVEL TUMOR SUPPRESSOR GENE, HIC-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER
                                                                                                                                                                                                     PEATURE:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 4616 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: P-38,3
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                               CLONE: HIC-1 polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: La Jolla
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                2211
297
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4225 Executive Square, Suite 1400
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                                                                                                        Score 44.6; DB Pred. No. 0.19;
                                                                                          Mismatches 104;
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                                                                                                                     Length 4616;
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US-08-452-567-1
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US-08-452-567-1/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/039003 (Div PD3664)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERITORY
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          FEATURE:
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NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
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                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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STATE: California
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                                                                                                                                                                                                                                                                                                     CLONE: HIC-1 polynucleotide
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nucleic acid
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25-MAY-1995
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                                                                                                                                                                                             Score 44.6; DB 2; Length 4616; Pred. No. 0.19;
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RESULT 11
US-08-452-427-1/c
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US-08-452-427-1
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Best Local Similarity 50.7
Matches 107; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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NAME/KEY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: UPPLICATION NUMBER: UP
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STATE: California
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CGGGGCTTAGGTCGGCGGGAGGAGGAGGTAAG
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US-09-085-407-1/c
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Best Local Similarity
Matches 107; Conserv
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APPLICATION NUMBER: US/08/340,203

FILING DATE: 15-NOV-1994

ATTORNEY/ACSINT INFORMATION:

NAME: Haile, Ph.D., Lisa A.

REGISTRATION NUMBER: 0-38,347

REPERENCE/DOCKET NUMBER: 07265/0390

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: : SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 422
STREET: 422
CITY: La Jolla
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baylin, Stephen B.
APPLICANT: Wales, Michele M.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE,
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line MOLECULE TYPE: DIMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: HIC-1 polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
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2031 TCGTGCTTCATCCAGCGATAGAGGAGACTAG 2001
                                                                2091
                                                                                               688 TGCAGCCCCGGGCAGAGGAGCCCCCGGCCCCAGGAGCCCCCGTTGGAGACCCCGCTCCCCC
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                                                                                                                                                                                               TCGTCGCCGTCGCCGCCCGCCCGGGCCCGGCCAGGCTAGCCAGGGTAGCGCGGCGGCGCC
                                 CGGGGCTTAGGTCGGCGGGAGAGGAGGTAAG
                                                                CGCTCGCTGGGGGAGCCGCTCCCGGCCCAGCTCGTCGCCATAGCTACCCAGGCCCGGC
                                                                                                                                4616 base pairs
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                                                                                                                                                                                                                                                                 0; Mismatches 104;
                                                                                                                                                                                                                                                                               Score 44.6; DB Pred. No. 0.19;
                               778
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                                                                                                                                                                                                                                                                                                Length 4616;
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APPLICANT: Goetinck, Paul F.
APPLICANT: Baciu, Peter C.
TITLE OF INVENTION: SYNDESMOS AND USES THEREOF
FILE REFERENCE: 10297-047001
CURRENT APPLICATION NUMBER: US/09/526,400
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,497
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 960
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US-09-526-400-3
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US-09-920-923B-36
                                                                                                US-09-526-400-3
Query Match
Best Local Similarity 50...
105; Conservative
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 36
LENGTH: 882
TYPE: NUMBER
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APPLICANT: Pasamontes, Luis
APPLICANT: Taygankov, Yuri
APPLICANT: Taygankov, Yuri
TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)
                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09526400 Patent No. 6566489 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                            TYPE: DNA
ORGANISM: Gallus
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ORGANISM: Unknown
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48.5%;
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                   Score 42.6; DB 4;
Pred. No. 0.34;
0; Mismatches 104;
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                       104;
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                                                       Length 960;
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Gaps

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RESULT 16
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US-09-526-400-1
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APPLICANT: Gostinck, Peter C.
APPLICANT: Baciu, Peter C.
TITLE OF INVENTION: SYNDESMS AND USES THERE
FILE REFERENCE: 10287-047001
CURRENT APPLICATION NUMBER: US/09/526,400
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,497
PRIOR FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 7
                                                                                                      Sequence 1, Application PC/TUS9208258
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC. and ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 105;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1182
TITLE OF INVENTION: PRODUCTION OF (NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                  848
                                                                                                                                                                                                                                                                                                   788
                                                                                                                                                                                                                                                                                                                                  806 CATGGACACGACTCTTGTCTACAAGCACCTGCCGGCTTCCGCCTTCTGCAGCCCCGCTGCC
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                                                                                       GENENTECH, INC. and VENTION: PRODUCTION
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ilarity 50.2%;
Conservative
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Pred. No. 0.37;
0; Mismatches 104;
                                                                                     STATE OF OREGON BY AND OF GPA NEUROTROPHIC FA
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US-09-270-767-13712/c
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Best Local Similarity
Matches 123; Conserv
                                  TYPE: DNA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Johnston, Sean REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1160
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; ORGANISM: Drosophila melanogaster US-09-270-767-13712
                                                                 Sequence 13712, Application US/09270767

Sequence 13712, Application US/09270767

Patent No. 6703491

Patent No. 6703491

Patent No. 6703491

Patent No. 6703491

APPLICANT: Homburger et al.

APPLICANT: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

SOPTWARE: PatentIn Ver. 2.0

SEQ ID NO 13712

SEQ ID NO 13712

LENGTH: 3096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1469 bases
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225)3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb |
COMPUTER: IBM PC compatible |
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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TELEFAX: 415/952-9881
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47.9%;
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Pred. No. 0.4;
0; Mismatches 134;
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APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: WHITE, OWEN R.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTMARE: PALENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 4403765
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US-09-103-840A-2
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Best Local Similarity
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Best Local Similarity
Matches 68; Conserv
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FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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           GGCCCTGCACCCCCTACTGTGTGTGGGTCCT 911
                                                      CGCCCCGCCGTTGCCGCCGACACCGCCGCTGCCACCCCATACCGCCGGTACCGCCGACACC 2956748
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Pred. No. 7.2;
0; Mismatches 243;
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RESULT 20
US-09-387-286-60
US-09-387-286-60; Application US/0938:
Patent No. 6544733;
GENERAL INFORMATION:
APPLICANT: Rommens, Caius M T
APPLICANT: Swords, Kathy M M
APPLICANT: Yan, Hua
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
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Local Similarity 45.0%;
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Pred. No. 7.2;
0; Mismatches 243;
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FILE REFERENCE: r gene patent
CURRENT APPLICATION NUMBER: US/09/387,286
CURRENT FILING DATE: 1999-08-31
CARLIER APPLICATION NUMBER: 60/098,402
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
FORCER: 2612
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3612
TYPE: DNA
ORGANISM: Nicotiana tabacum
                                                                                                                                                 TELEFAX: 617/248-7100 (INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 1941 base pairs
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND
REGISTRATION NUMBER: 27,8:
REFERENCE/DOCKET NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OPPERMANN, HERMANN APPLICANT: OZKAYNAK, ENGIN
                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                  TELEPHONE: 617/248-7000
ORGANISM: HU.
                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                FILING DATE: 1 CLASSIFICATION:
                                                                                                                                  TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Pred. No. 0.76;
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Patent No. 5670367
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                         APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                            TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
OTHER INFORMATION:
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CITY: A
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STRANDEDNESS:
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Alexandria
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507..1703
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51.6%;
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/product= "HOP2"
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RESULT 23
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 12;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,898
FILING DATE: 20 FEB 1998
ATTORNEY/AGENT INFORWATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 916/10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
                                                                                                                                                                                    OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
SOFTWARE: an ASCI file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,762A
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MIA HOROWITZ ET AL.
TITLE OF INVENTION: EH DOMAIN CONTAINING GENES AND PROTEINS NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
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                                                                                                                                                                                 FILING DATE:
                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                            Virginia
: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mark M. Friedman c/o Anthony Castorina
01 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.7%; Scor
3.1%; Pred.
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red. No. 1.
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LENGTH: 4411529
TYPE: DNA
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Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.7%;
Best Local Similarity 51.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA SEQUENCES FOR STRA:
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FLEISCHMAN, Robert D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1217931 CCGCGCCGCCACGGCCAGCGCCGGCGGCGATGCCCGTGCCGGCGGCGGCCGCCGCCGTCAC 1217872
1217751
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STRANDEDNESS: double
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CGCCG
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Pred. No. 1.9;
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Pred. No. 14;
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RESULT 25 US-09-621-976-17202

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SOFTWARE: Patent.pm
SEQ ID NO 17202
LENGTH: 364
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-621-976-16656
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SEQ ID NO 16656
LENGTH: 430
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APPLICANT: Dumas Milne Edwards, J.B.
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                                                             Matches
                                                                            Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                    ORGANISM: Homo sapiens
-09-621-976-16656
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APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                              APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OP INVENTION: ESTS and Encoded Human
FILE OPERENCE: GENSET.054PR2
CURRENT FILING DATE: 2000-07-21
RUMBER OF SEQ ID NOS: 19335
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                                                           Conservative
                                                                           2.6%;
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                                                     ; Score 40.6; DB
; Pred. No. 0.82;
87; Mismatches
                                                                                            DB 4;
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                                                         Gaps
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TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES
TITLE OF INVENTION: ENCODING FOR BIOSYMTHESIS OF
TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTANCE THE
FILE REFERENCE: 2653-40
CURRENT APPLICATION NUMBER: US/09/724,797
CURRENT FILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: 60/111,325
PRIOR FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
LENGTH: 3033
RESULT 28
US-08-881-857-1
; Sequence 1, Application US/08881857
; Patent No. 5919660
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; LOCATION: (1)...(3033)
US-09-724-797-81
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Patent No. 6733998
GENERAL INFORMATION:
APPLICANT: Jon S. THORSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bacteria FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                   1777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 SGGSCYKKKKKGKKGSCCMRSYMMCCYYYKRARRMMWKGGSCMMYTKRMMRRMCCCCMRR 197
                                                                                                                                                                                                                                                                                                                                                                      GCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCCCAGCC 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGCCCGGCTCAACAGGTCCGCGCAGGCGATGCGGACCAGCTCCCGGCGGCGCAGCGCG 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGCCCTGCACCCCTACTGTGTGTGGGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTG 939
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                                                                                                                                        CGAG 1714
                                                                                                                                                                                                                                                                              CCGCCCGCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGCTCTGC 1179
                                                                                                                                                                                                                                                                                                                             GCGCCTCCGGCTCGCGGGCCAGCAGGTCGGCGGCGTAGCGGGAGGAGGAGCACCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCGCAGAGCACCCCGCTCGGCCGGGGGGGTCAACTCGCTCTCCTCGGCCAGCATCCGCA 1838
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                                                                                                                                                                                                                                   CCAGCCGGCCGGCCCCGGAGTCGCGCAGCAGGCAGGTACCAGGGCGTGCTGC
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Pred. No. 1.8;
0; Mismatches 156;
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ENERAL INFORMATION:

APPLICANT:

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                                                                                                                                                                                                                                                                                                                 RESULT 29
                                                                   APPLICANT: KIKLY, KRISTINE K.
APPLICANT: GROSS, MITCHELL S.
APPLICANT: HURLE, MARK ROBERT
TITLE OF INVENTION: HUMAN REQUIEM
FILE REFERENCE: ATG-50013-1
CURRENT APPLICATION NUMBER: US/09/233,342A
CURRENT FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: 08/881,857
PRIOR APPLICATION NUMBER: 08/881,857
PRIOR FILING DATE: 1997-06-24
                                                                                                                                                                                                                                        Sequence 1, Application US/09233342A Patent No. 6207803 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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FILING DATE: 24-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,229
FILING DATE: 26-JUN-1996
ATTORNEY/AGENT INFORMATION:
DATE: DESCRIPT DATE:
                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 846169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: ATT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN REQUIEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1556 base par
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 59.(
les 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 610-407-0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              1073
                                                                                                                                                                                                                                                                                                                                                                     1133 CACCCCGTCCATGTCTGAGCCCCCTGAAGGAAGTTGGAGCTGCCACCTGTGTCTGGA 1189
                                                                                                                                                                                                                                                                                                                                                                                                       19482
 SEQ ID NOS:
FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATGACCACTTGCTCTTCTGTGATGACTGCGATCGTGGCTACCACATGTACTGTCT 1132
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: GROSS, MITCHEL
: HURLE, MARK R
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                                    1996-06-26
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Windows Version 3.0
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                                                       60/021,299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.2; DB 2; Length 1556;
Pred. No. 1.6;
0; Mismatches 48; Indels 0
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US-09-620-312D-389/c
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LENGTH: 1556
                                                                                                                                                                                                                                                                                                                  SOFTWARE: pt_FL_genes Version 1.0 SEQ ID NO 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.0
Best Local Similarity 59.0
Matches 69; Conservative
                                                                                                                                   Matches 105;
                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 389,
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic /
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (25)..(1197)
                                                                                                                                                                                                                                                 LENGTH: 1682
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
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ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT:
                               1024 CAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTGA 1083
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                                                                                                614 GTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCCA 670
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Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
                                                                GCACGGAGCACTGGCCCGGCATTCGCCGCTCCGTCGCCGCCCAGGGCGCCTCCTCCTCCG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang,
CCCCGGTCGCATCTCGCAGCAGCTCCGCTACACCCTGGGCGCCCCGGCGGAGGCACCGGGA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Xue, Aidong J.
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Wang, Zhiwei
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ndi, Vinod
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No. 6569662el Nucleic Acids
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                                                                                                                                               2.6%;
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                                                                                                                               Score 40.2; DB 4;
pred. No. 1.6;
0; Mismatches 108;
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Pred. No. 1.6;
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                                                                                                                                                                 Length 1682;
                                                                                                                                 Indels
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RESULT 32
US-09-338-125-9
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COMPUTER: IBM Compactive
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION UNDERS: US/08/969,10
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
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                                                                                                                                                                                                                                                                                                                                           US-08-969-106-9
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GENERAL INFORMATION:
 GENERAL INFORMATION:
APPLICANT: Yang, M
APPLICANT: Nandaba
APPLICANT: Schulz,
                                                            Sequence 9, Application US/09338125 Patent No. 6521412
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                Matches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2399 base pairs
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TITLE OF INVENTION: CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: Z12-869-9741
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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Yang, M.
Nandabalan,
Schulz, V.
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Nandabalan,
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Pred. No. 1.8;
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; FEATURE:
; NAME/KBY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549516H1
US-09-313-294A-604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-338-125-9
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                                                                                                            SOFTWARE: PE
SEQ ID NO 604
LENGTH: 293
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APPLICANT: Lalgudi
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                                                                              APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OP INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORWATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,87
                                                                          TYPE: DNA
ORGANISM: Zea mays
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/338,125
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ZIP: 100
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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1155 Avenue of the Amer.
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US-09-252-991A-11986
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US-09-252-991A-11956
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PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11986
LENGTH: 762
                                                                                                                          Sequence 11956, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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APPLICANT: Marc J.
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
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1998-02-18
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50.5%;
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Pred. No.
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APPLICANT: Reynolds, Paul R.
APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5.5
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; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-680-506-5
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11956
LENGTH: 1125
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                      Query Match 2.6%; Score 39.6; Best Local Similarity 44.9%; Pred. No. 1. Matches 150; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Applic Patent No. 6008013
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                     1225
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                                                        Application US/08680506C
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Pred. No. 1.
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GENERAL INFORMATION:
APPLICANT: Reynolds, Paul R.
APPLICANT: Reynolds, Paul R.
APPLICANT: Reynolds, CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATEINT NOS: 18
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SOFTWARE: PATEINT NOS: 18
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US-08-680-506-6
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US-08-680-506-8
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Patent No. 6008013
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Best Local Similarity 44.9%;
Matches 150; Conservative
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Patent No. 600801;
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ORGANISM: Gallus gallus
     TYPE: DNA
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Pred. No. 2.
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; ORGANISM: Gallus
US-08-680-506-4
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APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 150; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
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Pred. No. 2.5;
0; Mismatches 184;
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Pred. No. 2.2;
0; Mismatches 184;
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US-08-785-310A-4/c
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                                                                                                                                                                                                                                                                                                                     Query Match 2.6%;
Best Local Similarity 50.4%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        -08-785-310A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 343-7274.
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
100 hare palife
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION UNDER: 36,627
REFERENCE/DOCKET NUMBER: UTSD
TELECOMUNICATION INFORMATION:
TELECHONE: (415) 343-4341
TELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: McKnight, Steven L.
APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS: 8 TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 21-JAN-199
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Policy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4184 base pairs
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                               515 CC 516
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                                                                                            455 GAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTGCATGGGCGTCTCTTG
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CC 10
                                                                                                                                                                                          GGCAGCGGCAATCTTGAAAGCTTCTGTCCGGGCACGCAGTACCCCTCTAGCACCCTCGG
                                                                                                                                                                                                                        AGACCAGATGGATGGGGAAACAGGT-GGTCAGGGCAGAATTTCAGGCCCTGGCAGCATGGG
                                                                                                                                                                                                                                                          CACTCTCCAGGCGTCCCGGGCTCCCTACGCTTCGGGATGCCTGCGGTGGGGGCTCTGGAAG
                                                              GAGCCCACCGTCTGTCTGGCTGCAGCGGTTGGCAGGACCCCGAAGCCCCAGGGCGGCTCGTG
                                                                                                                            AGGACCCCGAATCCCGATGTTTGGGGTGCCTAGTCCTCTCTTTGGCGAGCAGCTCCGG
                                                                                                                                                       AGCAGGGCAGAGACTGGGGAGTTCAGGTACCCAGAGATGCTGCTGGGGGAGCTGTTTTGG
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US-09-679-279-1/c
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US-08-680-506-2
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                                               SOFTWARE:
SEQ ID NO 1
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LENGTH: 5027
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               LENGTH: 47
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GENERAL INFORMATION:
APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                          1285 CCCAGATGGCCGGGACATGCAGCTCTGATGAGAG 1318
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                                                                                                                                  GCATCCTGCAGTGGGCCATCCAGAGCATGGCCGGTCCGGCGGCCCCCTTCCCCTGAC 1284
                                                                                                                                                                                                                        CGCCGTGCCGCTGCCTGTCGTCGCCGCTTCTGGTAGCGGTGGCGAGCGCCGGGCTGG
CGCTGGCCGCCTGGCCGATGTGGTACGAGGAGAG
                                                                                        AGCTCCGCCGCCGCCACGGCACCCGCTACCCCACGGCCGAAATCCGCCGCC
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ilarity 44.9%;
Conservative
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  418
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ESULT 42
S-09-679-279-1/c
Sequence 1, Application US/09679279
Sequence 1, Application US/09679279
Patent No. 6524841
GENERAL INFORMATION:
APPLICANT: WcDaniel, Robert
APPLICANT: Volchegureky, Yanina
TITLE OF INVENTION: Genes and Uses Thereof
FILE REFERENCE: 300622004700
CURRENT PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US/09/679,279
CURRENT FILING DATE: 2000-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 34
PRIOR FILING DATE: 2000-03-17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 47981
TYPE: DNA
ORGANISM: Micromonospora megalomicea

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NAME/KEY: misc feature
LOCATION: (17155)...(17694)
OTHER INFORMATION: megAI, KRI
NAME/KEY: misc feature
LOCATION: (17947)...(18207)
OTHER INFORMATION: megAI, ACPI
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (12505)...(13470)
OTHER INFORMATION: megAI, AT-L
NAME/KEY: misc feature
LOCATION: (13576)...(13791)
OTHER INFORMATION: megAI, ACP-L
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OTHER INFORMATION: 7
OTHER INFORMATION: 8
NAME/KEY: CDS
                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (15427)...(16476)
OTHER INFORMATION: megAI, ATI
                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (13849)...(15126)
OTHER INFORMATION: megAI, KS1
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OTHER INFORMATION: megBIV,
OTHER INFORMATION: TDP-4-ke
OTHER INFORMATION: SEQ ID N
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: CDS
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (12181)...(22821)
OTHER INFORMATION: megAI; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
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INFORMATION: SEQ ID NO: 2=
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N: megDI, rhodosaminyl transferase (eryCIII homolog),
N: TDP-megosamine glycosyltransferase;
N: SEQ ID NO: 4= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...(10479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ... (6595)
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SEQ ID
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SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  megDII, deoxysugar transaminase (eryCI, DnrJ homolog), TDP-3-keto-6-deoxyhexose 3-aminotransaminase; SEQ ID NO: 6= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         megBIV, TDP-hexose 4-ketoreductase,
TDP-4-keto-6-deoxyhexose 4-ketoreductase;
SEQ ID NO: 12= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . (8206)
megDV, TDP-hexose 4-ketoreductase (eryBIV, dnmV homolog)
TDP-4-keto-6-deoxyhexose 4-ketoreductase;
SEQ ID NO NO: 9= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             megDIV, TDP-4-keto-6-deoxyglucose 3,5-epimerase TDP-4-keto-6-deoxyhexose 3,5-epimerase; SEQ ID NO: 8= translated amino acid sequence
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SEQ ID NO: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           megBII-1(megDVII), TDP-4-keto-L-6-deoxy-hexose
SEQ ID NO: 10= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mycarosyl transferase, mycarose glycosyltransferase, NO: 11= translated amino acid sequence
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NO: 7= translated amino acid sequence
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NAME/KEY: misc_feature
LOCATION: (28897)...(29931)
OTHER INFORMATION: megAII, AT4
NAME/KEY: misc_feature
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LOCATION: (24544)...(25581)
OTHER INFORMATION: megAII,
                                                                                NAME/KEY: misc_feature
LOCATION: (42168)...(42425)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: megAIII, NAME/KEY: misc feature LOCATION: (39795)...(40811)
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (38187)...(39470)
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: megAIII, NAME/KEY: misc feature LOCATION: (37860)...(38120) OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc fe
LOCATION: (37068)
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LOCATION: (35385)...(36419)
OTHER INFORMATION: megAIII,
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OTHER INFORMATION: megAIII,
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LOCATION: (33052)...(33312)
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OTHER INFORMATION: megAII, DH4
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LOCATION: (26998)...(27258)
OTHER_INFORMATION: megAII, ACP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (26230)...(26733)
OTHER INFORMATION: megAII, KR3 (inactive)
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NAME/KEY: misc_feature
                                                                                                                                                                              LOCATION: (41406)...(41936)
OTHER INFORMATION: megAIII,
                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                     OTHER INFORMATION: megAIII,
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LOCATION: (33780)
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OTHER INFORMATION: megAIII;
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LOCATION: (27393)
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OTHER INFORMATION: megAII; SEQ ID NO: 14= translated amino acid sequence
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                                                           NAME/KEY:
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LOCATION: (29953)...(3
                           misc_fe (42585)
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acid sequence

Floppy disk

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US-08-998-416-723; Sequence 723, Application US/08998416; Patent No. 6239264
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Best Local Simi
Matches 155;
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OTHER INFORMATION: n
OTHER INFORMATION: 1
OTHER INFORMATION: 5
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OTHER INFORMATION: megCIII, desosaminyl transferase, desosamine glycosyltransferase
OTHER INFORMATION: SEQ ID NO: 17= translated amino acid sequence
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OTHER INFORMATION: megF, C-6 hydroxylase; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (46660)...(47403)
OTHER INFORMATION: megH, TEII; SEQ ID NO: 19= translated amino acid
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APPLICANT:
APPLICANT:
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LOCATION: (43268)...(44344)
                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                          APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES
TITLE OF INVENTION: AND USES THEREOF
COMPUTER READABLE FORM:
                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                     Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                              Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                      Mohr, Christine
                                    USA
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TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
SEQ ID NO: 18= translated amino acid sequence
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SEQ ID NO:
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Pred. No. 7.
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Mismatches
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                                                                                                                                                                                                                                       sequence 2, Application US/09655270A Patent No. 6329151
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rouvier
SEQ ID NO 2
LENGTH: 1596
                                                                                                                           PILE REFERENCE: BC1011 US NA CURRENT APPLICATION NUMBER: US/09/655,270A CURRENT FILING DATE: 2000-09-05 PRIOR ADDITOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                               PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
PRIOR APPLICATION NUMBER: 60/152,542
PRIOR FILING DATE: 1999-September-03
NUMBER OF SEQ ID NOS: 37
SOPTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 24-DEC-199
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 675 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: PatentIn Release #1.0.
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COMPUTER: II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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ilarity 46.3%;
Conservative
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Pred. No. 1.9;
0; Mismatches 151;
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; Sequence 2, Application US/0995597; Patent No. 6461856; GENERAL INFORMATION:
APPLICANT: ROUVIER, PIERRE E
APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric Ac
FILE REFERENCE: BC1022 US NA
CURRENT FILING DATE: 2001-09-17;
PRIOR APPLICATION NUMBER: US/09/955,597;
PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
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US-09-955-597-2
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; ORGANISM: Rhodococcus erythropolis HL
US-09-651-941-2
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US-09-651-941-2
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US-09-655-270A-2
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Best Local Similarity
Matches 92; Conserv
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SEQ ID NO 2
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APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
FILE REFERENCE: BC1022 US NA
CURRENT APPLICATION NUMBER: US/09/651,941
CURRENT FILING DATE: 2000-08-31
REFOR APPLICATION NUMBER: 60/152,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
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ilarity 51.1%;
Conservative
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Pred. No. 2.8;
0; Mismatches
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                                                                                           Degradation
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; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-955-597-2
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US-09-655-270A-1
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                                                                     US-09-651-941-1
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                                                                                    RESULT 48
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CURRENT APPLICATION NUMBER: US/09/655,2
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
PRIOR APPLICATION NUMBER: 60/152,542
PRIOR FILING DATE: 1999-September-03
NUMBER OF SEQ ID NOS: 37
NUMBER OF SEQ ID NOS: 37
Sequence 1, Application US/09651941
PATENT NO. 635470
GENERAL INFORMATION:
APPLICANT: ROUVIER, PIERRE E
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 12508
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SOFTWARE: Microsoft Office
SEQ ID NO 2
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Best Local
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Best Local Similarity 51.1%;
Matches 92; Conservative
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TITLE OF INVENTION: High Density Sampling
FILE REFERENCE: BC1011 US NA
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Pred. No. 5.7;
O; Mismatches
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Pred. No. 2.8;
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APPLICANT: APPLICANT: WALTERS, APPLICANT: RAINER, TITLE OF INVENTION:

PIERRE DANA M

RUSS
Genes Encoding Picric Acid Degradation

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RESULT 50
US-09-222-991A-12051/c
; Sequence 12051, Application US/09252991A
; Patent No. 6551795
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; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-651-941-1
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                                                                                                                                                                                                                                                                                                                                                                                            US-09-955-597-1
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/955,597
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 12523
TYPE: NAT
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NUMBER OF SEQ ID NOS: 28
SOFTWARE: MicroBoft Office 97
SEQ ID NO 1
LENGTH: 12523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09955597 Patent No. 6461856 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric
FILE REFERENCE: BC1022 US NA
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CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,545
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Rhodococcus erythropolis HL PM-1
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Pred. No. 5.7;
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Pred. No. 5.7;
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GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO INTELLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

INUMBER: US 60/094,190

PRIOR APPLICATION SATISTICIONAL SEGUID NO 11993

LENGTH: 564

TYPE: DNA

DEGINTAN: DEGINTANCES APPLICATIONS
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LENGTH: 531
TYPE: DNA
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Patent No. 6551795
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ABBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
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                                         662 CTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCGGCCCCAGGA 721
                                                                                                                  602 CCTGGCCTGCTCCCCCTCCGGCAGATCCCCCAGTGGGAGCTTGGAGGTGCTCCAG 661
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                                                                                    CCTGTTCGCCCTGACCCTGCACGGAGCGGTGATCCATTGGCTGAGCCAGCAGAGAACCCCC
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llarity 50.3%;
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Pred. No. 2
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Pred. No.
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US-09-252-991A-14041
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11962
                                                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 14041
                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                Sequence 14041, Application US/09252991A Patent No. 6551795
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Best Local :
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                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THEDADDITYTON
                                                                                                         PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                           APPLICANT:
                                  LENGTH: 64
TYPE: DNA
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ORGANISM: Pseudomonas
                  ORGANISM: Pseudomonas aeruginosa
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RESULT 55
US-09-252-991A-13605
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US-09-252-991A-13744/c
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APPLICANT: Marc J. R
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                Sequence 13605, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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SEQ ID NO 13744
LENGTH: 708
TYPE: DNA
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Best Local Similarity
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Best Local Similarity
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1163
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No.
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Pred. No. 2.7;
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEU
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13494
LENGTH: 984
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13494
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US-09-252-991A-13494
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PRIOR APPLICATION NUMBER: US O
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 33142
SEQ ID NO 13605
LENGTH: 804
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Patent No. 6551795
GENERAL INFORMATION:
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Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 118; Conserv
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TCCAAAGGCGGCGAACCTGCCGGCTGTCGATCAGGTGCTGGCTTTCGAGCAGGCCCTCGG
                                                         AGGTGCGGACATGAGCCGCATCGACACGCCGCCGGGATTCGCCGTCTATCCGTCGGCCAG
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ilarity 47.2%;
Conservative
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Pred. No. 3
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Pred. No. 2.
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4137
LENGTH: 1104
                                                                                                                                                                        RESULT 58
US-09-252-991A-4071
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Sequence 4071, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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Best Local Similarity
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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MATC J. Rubenfield et al.
MATC J. RUBENFIELD ALID AMINO ACID SEQUENCES RELATING
VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
VENTION: NOTATION FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 3.1;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4071
LENGTH: 1275
TYPE: DNA
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-4071
                                                                                                                                                 FILE REFERENCE: 210121.538

(CURRENT APPLICATION NUMBER: US/09/894,998A)

(CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 35

LENGTH: 2481

TYPE: DNA

ORGANISM: HSV-2

US-09-894-998A-35
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US-09-894-998A-35/c
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GENERAL INFORMATION:
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Best Local Similarity
Matches 160; Conserv
   Query Match
Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hosken, Nancy Ann
APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
APPLICANT: McGowan, Patrick
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
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   Score 38.8; DI
Pred. No. 4.1;
O; Mismatches
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Pred. No. 3.3;
0; Mismatches 202;
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       177;
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RESULT 61
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                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQ ID NO 8
; LENGTH: 11958
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09134246B
Patent No. 6207377
General Information:
Applicant: Wayne, Jay
Applicant: Wayne, Jay
Applicant: Yay, Shuang-yong
TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid
TITLE OF INVENTION: Replication Origins
FILE REFERENCE: Thermus Shuttle Vector
CURRENT APPLICATION NUMBER: US/09/134,246B
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                  Matches
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Best Local 9
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                                                                                                                                                                                                                                                                                                                               Match 2.5%;
Local Similarity 50.3%;
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                                                                                                                                                                                         GAGGÉTÉCGGGTGATCTCCTGGTGGAGGTTGAGGTTCCCCTGAAGGACATCTACGATCAC 8805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACA 828
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                                                                                            GCTCCCCCC
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                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                              DB 3;
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                                                                                                                                                                                                                                                                                                                                               Length 11958;
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Sequence 64, Application US/09765400 Patent No. 6691568 GENERAL INFORMATION:

APPLICANT: Ghazal,

Peter

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HAPPLICANT: Huang, Huang
ITITLE OF INVENTION: Generation of Human Cyto
ITITLE OF INVENTION: Recombinants
FILE REFERENCE: 98,299
CURRENT APPLICATION NUMBER: US/09/765,400
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 64
LENGTH: 229354
TYPE: DNA
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US-09-705-400-64
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APPLICANT: Huang, Huang
TITLE OF INVENTION: Generation of Human Cyto
TITLE OF INVENTION: Recombinants
FILE REFERENCE: 98,299
CURRENT APPLICATION NUMBER: US/09/705,400
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-765-400-64
                                                                                                                              US-09-705-400-64
                                                              Query Match
Best Local S
Matches 124
                                                                                                                                                                                                                    SOFTHALL
SEQ ID NO 64
TWIGHTH: 229354
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 64, Application US/09705400 Patent No. 6692954 GENERAL INFORMATION:
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Best Local Similarity
Matches 124; Conserv
                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                   LENGTH: 229354
TYPE: DNA
ORGANISM: Human cytomegalovirus
                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Human cytomegalovirus strain AD169 (GenBank X17403.1)
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                                                                                                                                                                              FEATURE:
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93012
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                  946 GCGGGGTTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCC 1005
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                                                                               Similarity
GCGCAGTCCGCGGCAGGGTTCCCGGCCGTGCCGCTCCGCACGCTGCGCCCCGCTCCCGCC
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49.8%;
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49.8%;
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                                                                             Score 38.6;
Pred. No. 21;
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Pred. No. 21;
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                      Human Cytomegalovirus Yeast Artficial Chromosome
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                                                                                                                                             strain AD169 (GenBank X17403.1)
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                                                              Indels
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RESULT 64
US-09-077-940A-3
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; NAME/KEY: CDS
; LOCATION: (1)...(1683)
US-09-724-797-21
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US-09-724-797-21
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; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Bacteria
Sequence 3, Application US/09077940A
Patent No. 6576441
GENERAL INFORMATION:
APPLICANT: KIMURA, TOTU et al.
TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND
FILE REFERENCE: 0020-4426P
CURRENT APPLICATION NUMBER: US/09/077,940A
CURRENT FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: JON S. THORSON
TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES
TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09724797 Patent No. 6733998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2653-40
CURRENT APPLICATION NUMBER: US/09/724,797
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/111,325
PRIOR FILING DATE: 1998-12-07
NUMBER OF SEO ID NOS: 95
NUMBER OF SEO ID NOS: 95
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93251 CCGGCCGGG 93255
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48.6%;
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GENE

ENCODING

THE SAME

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RESULT 65
US-10-140-002-543
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                                                                                                                                                                                                                                                                                                           Sequence 543, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
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SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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APPLICANT:
APPLICANT:
                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-077-940A-3
         APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
                                                                                                                                                                                                                       APPLICANT:
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LOCATION: (39)..(2
OTHER INFORMATION:
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NAME/KEY: 5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: 3'UTR
LOCATION: (2706)..(3524)
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OTHER INFORMATION:
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Local Similarity 47.0%;
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                                                                                                                                            Gao, wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                              Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCCACCCGTGGAGACCCCGCTCCCCC 747
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Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                 DeForge, Laura
                                                                                                                  Stewart, Timothy A.
                                                                                                                                  Smith, Victoria
                                                                                                                                                                                                                                                   Desnoyers, Luc
                                                                                                                                                                                                                                                                                 Beresini, Maureen
                                                                                                                                                                                                                                       Filvaroff,Ellen
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NUMBER: US/10/140,002
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                                          POLYPEPTIDES
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CURRENT FILING DATE: 2002-
FRIOR Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 543
ENGTH: 3721
TYPE: DNA
ORGANISM: HOMO Sapien
US-10-140-002-543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 66
US-09-191-171-7/c
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Patent No. 6149909
Patent No. 6149909 6143294
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Best Local Similarity
Matches 154; Conserv
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, W
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,171
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 23-JUN-1995
                                                                                                                                                                                                                                                                                                                              APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: HOPMOOD, JOHN J.
TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE
TITLE OF INVENTION: SEQUENCES ENCODING SAME
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          ADDRESSEE: SCULLY SCOTT MURPHY
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2167
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nilarity 47.0%;
Conservative
                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamish
Donald
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Pred. No. 5
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                                                                                                                          Version
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RESULT 67
US-09-385-707-7/c
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                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: SCOTT,
APPLICANT: ANSON, I
APPLICANT: ORSBORN,
APPLICANT: NELSON,
                                                                                                                                                                                                                                           Sequence 7, Application US/09385707 Patent No. 6238662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 4480 base pairs
                                                                           APPLICANT: ORSBORN, Annette M.
APPLICANT: NELSON, Paul V.
APPLICANT: CLEMENTS, Peter R.
APPLICANT: MORRIS, Charles P.
APPLICANT: HOPWOOD, John J.
TITLE OF INVENTION: SYNTHETIC NITITLE OF INVENTION: SEQUENCES EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8978Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 12-NOV-1992
PRIOR APPLICATION NUMBER: US 08/084,254
                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
STREET:
CITY: G
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 516-742-43
TELEFAX: 516-742-4366
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                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                            2380
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                                                                                                                                                                                                                                                                                                                                             CCCCAGCGGCCCCGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                            TCCCCGCAGCGGGCCTTCGCAGGAGCCGCTCCCCAGCCTGGAGGGCCCTGGCCCGGCCCA 2321
             E: SCULLY SCOTT MURPHY & PRESSER
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Pred. No. 6.3;
                                                                              ALPHA-L-IDURONIDASE AND ENCODING SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 4480;
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                                                                                                                                                             RESULT 68
US-09-639-696C-6/c
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                                                                         Sequence 6, Application US/09639696C
PATENT NO. 6524835
GENERAL INFORMATION:
APPLICANT: SCOTT, Hamish S.
ANSON, Donald S.
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US-09-385-707-7
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Best Local S
Matches 150
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COUNTRY: USA
ZIP: 11530
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/385,707 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                        2558
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2320 CCCCAGCGGCCCCGGCTC 2303
                                                                                                                                                   2440 TCCCCAGGCCCGCCACGCGAGGCCGACCCCGGGAAGCGCGCGCGGCTGGAGGAAGTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                      592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             150;
                                                                                                 ACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTGCACC 891
                                                                                                                                                                                                                                                                                                        GCTGCTCCTCAT--CTGCGGGGGGGGGGGGGGGGCCGTCGCCGTGGGGTCGTTGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                    GGACGCCCACCGTGTGGTTGCTGTCCAGGACGGTCCCGGCCTGCGACACTTCGGCCCAGA
                                   CCCTACTGTGTGGGTC 909
                                                                                                                                                                                       AGGTAAGAGGTCCACCTGGGGAACCCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGC 831
                                                                                                                                                                                                                              GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCC
                                                                         TCCCCGCAGCGGGGCCTTCGCAGGAGCCGCTCCCCAGCCTGGAGGGCCCTGGCCCGGCCCA 2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4480 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38.4; D)
Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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ORSBORN, Annette M.
NELSCON, Paul V.
CLEMENTS, Peter R.
MORRIS, Charles P.
HOPWOOD, John J.

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US-09-639-696C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/084,254
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               4198
                                                                                                                                                                                                                                                       4258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 6238 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               4316 GCTGCTCCTCAT--CTGCGGGGCGGGGGGGGGCCGTCGCCGCGTGGGGTCGTTGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                       4376 GGACGCCCACCGTGTGGTTGCTGTCCAGGACGGTCCCGGCCTGCGACACTTCGGCCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON PEABODY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC SEQUENCES ENCODING SAME
                                                                     712
    892 CCCTACTGTGTGTGGGTC 909
                                                                                                                                                                                                               772
                                                                                                                                                                                                                                                                                                                                                                                            652
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                                                                                                                                                                                                                                                       CGCCCCCGACCCAGGGCCGGGCCTCCCACCACTCGCTCCCCCTCCCCTTGGTGAAGGAG
                                                                                                                                                             TCCCCAGGCCCCGCCACGCGGAGGCCCGACCCCGGGAAGCGCGGCTGGAGGAAGTGCGC
                                                                                                                                                                                                          AGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGC
                                                                                                                                                                                                                                                                                                  GGCCCAGGAGCCACCCGTGGAGACCCCCGCTCCCCCCGGGGCTTAGGTCGGCGGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Pokalsky, Ann R.
REGISTRATION NUMBER: 34,697
REFERENCE/DOCKET NUMBER: 2249/304
                                                                                                               ACCIGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCCTGCACC 891
                                                                                                                                                                                                                                                                                                                                                                                          GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: AU PK9490/91
FILING DATE: 14-NOV-1991
APPLICATION NUMBER: AU PCT/AU92/00611
FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/191,171
FILING DATE: 13-NOV-1998
APPLICATION NUMBER: US 08/494,104
FILING DATE: 23-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 990 Stewart Avenue CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/639,696C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 516-832-7555
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Pred. No. 7.
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                                               US-09-252-991A-6641
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
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SEQ ID NO 6674
LENGTH: 1260
                                                                                                               SEQ ID NO 6641
LENGTH: 2163
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6641, Application US/09252991A Patent No. 6551795
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Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                     ORGANISM: Pseudomonas
                                                                                          TYPE: DNA
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  2.5%;
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Pred. No. 4.6;
0; Mismatches 138;
  Score 38.2;
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    Length 2163;
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RESULT 71
US-08-289-112-1
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Patent No. 5688640
 Query Match 2.5%;
Best Local Similarity 51.5%;
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BATENIA PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/289,112

FILING DATE: 10-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REGISTRATION NUMBER: 32,165

REGISTRATION INFORMATION:

TELEPHONE: 713-787-1400

TELEPHONE: 713-787-1400

TELEPAX: 720-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Yanagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Arnold, Wh
STREET: P.O. Box 4433
                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                 NAME/KBY:
                                                                                 LOCATION:
                                                                                                                                                                                                ENGTH:
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                                                                                                                                                                                              2889 base pairs
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VENTION: Endothelin Converting Enzyme-1: A
VENTION: Membrane-Bound Metalloprotease That Cataly
VENTION: Proteolytic Activation of Big Endothelin-1
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Score 38.2; DB Pred. No. 6.1; 0; Mismatches
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US-09-103-840A-2
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APPLICANT: WHITE, Owen R.
APPLICANT: WRITER, Olaire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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US-09-103-840A-2/c
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Best Local Similarity
Matches 187; Conserv
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INFORMATION: "n" bases at various positions throughout the
INFORMATION: represent a, t, c or g
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    Application US/09103840A
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                                               GGCCCGGGACGGCCTGCACATCCTGCTCAGGAGACGTGACCCCAGCCCCTG 1095
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Pred. No. 58;
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REESTRATION NUMBER: DFCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08458568A Patent No. 5821339
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Best Local
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APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
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APPLICATION NUMBER: US/08/458,568A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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STREET: One Liberty Place, 46th floor
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220
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                                                                TCGCCCTCCGCCTGCGCGTCACCGCGGAGCACCTGGCGCGCCTGCGACGCGCGG 221
                                                                                                GGCCCCCAGCCCCGCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGA 1168
                                                                                                                                                                 GGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTGACCCCCAGCCCCTGTGGAGGGGGGTGCT 1108
GC 219
                                                                                                                                   CGGGGGGGGGGGCTGACCCCTCCCACCCCCCCCTCGCGCCCTTCCGCCCTTCCGCCGCCGCCCC
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Herpes Simplex Virus Type
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Pred. No. 4.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                                          DB 1;
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US-08-196-218-31
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                                           Sequence 31, Application US/08196218 Patent No. 5614619 GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION UNDER: PCT/US91/06532
PILING DATE: 19910910
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GRUBER, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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                APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy
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   APPLICANT:
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STATE: Illinois
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                                                                                                                                                        GC 588
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Piepersberg, Wolfgang
Stockmann, Michael
Taleghani, Kampiz Mansouri
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Pred. No. 5
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                                                                                                                              RESULT 76
US-08-681-953-31
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US-08-196-218-31
Sequence 31, Application US/08681953
Patent No. 5710032
GENERAL INFORMATION:
APPLICANT: Piepersberg, Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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NAME/KEY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,;
REFERENCE/DOCKET NUMBER:
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TITLE OF INVENTION:
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TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Grabley, Susanne
Sichel, Petra
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ilarity 51.8%;
Conservative
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416..1531
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3..401
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Pred. No. 6.6;
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US-08-681-953-31
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/196,218
FILING DATE: 25-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 02481.1372
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Brau, Barbara
TITLE OF INVENTION: Secon
TITLE OF INVENTION: Fron
TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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NAME/KEY:
LOCATION:
FEATURE:
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COMPUTER READABLE FORM:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                             1028
 2148
                                                                                                                            2028
                                                                                                                                                         968 GGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCAGC 1027
                                                                                                                                                                                        l Similarity
86; Conserv
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                                                                                                                           GGAGAAGCCGTGGCAGCCGCGACCATGGCCCTGATCGGGGTCTACTTCTTCACCGC 2087
                             CGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTGACCCC 1087
                                                             CGCCATCCACCAGGCGGTGGCGGCCATCTCGCCCAGCAGCCGCGGCGAACTGGAGATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2634 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Dunner
1300 I Street, N.W.
                                                                                                                                                                                          Conservative
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Grabley, Susanne
Sichel, Petra
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Taleghani, Kampiz Mansouri
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                                                                                                                                                                                                                                                                                                                     CDS
416..1531
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1561..2625
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                                                                                                                                                                                                      Score 38; DB
Pred. No. 6.6;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                      DB 1; Length 2634;
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2193
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Best Local Similarity
"hes 77; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08458568A Patent No. 5821339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/341,550
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: PCT/US98/00840
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/035,955
PRIOR FILING DATE: 1997-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: SCR2177S
CURRENT APPLICATION NUMBER: US/09/613,182
CURRENT FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mayfield, Stephen
TITLE OF INVENTION: RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/069,400 PRIOR FILING DATE: 1997-12-12 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (197)..(2065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Chlamydomonas reinhardtii
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Composition TITLE OF INVENTION: Infections NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schaffer, Priscilla A. APPLICANT: Yeh, Lily
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             STREET: One LIDELLY CITY: Philadelphia
                                  APPLICATION NUMBER: US/08 FILING DATE: 02-JUNE-1995
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                              ADDRESSEE:
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NO. 6294653
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One Liberty Place, 46th floor
                                                                                                                                                                                                                USA
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54.2%;
                                                                                                                                                                                                                                                                                                                                                                        Compositions and Methods for Treatment of Herpesvirus
                                                         US/08/458,568A
                                                                                                                                                                                                                                                                                          Washburn, Kurtz, Mackiewicz & No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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; LENGTH: 13842
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-30
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US-09-105-537-30
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type
US-08-458-568A-11
                                                                                                                                                                                                                                                                                                                                                    Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, I
APPLICANT: Liu, H.
                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 92; Conserv
                                                                  Matches
                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30,
                                                                                                                                                                                                                                APPLICANT: Zhue, Y.
APPLICANT: Zhue, Y.
APPLICANT: Zhue, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT FAPPLICATION NUMBER: US/09/105,537A
CURRENT FILLING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12001 base pai
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI-0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 05-MAY CLASSIFICATION: 435
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TOPOLOGY: lir
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9891 GCGCGGCCGCTCATGCAGGAGCTGCCCGCCGGTGGCGCGATGCTCGCCGTCCAGGCCGC 9950
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                    440 GGGGAGCTGTTTTGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTG 499
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                                                                  87;
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ilarity 50.5%;
Conservative
                                                                  Conservative
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                                                                  0;
                                                                  Score 37.8; DI
Pred. No. 13;
0; Mismatches
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Pred. No. 11;
0; Mismatches 9
                                                                                               DB 3;
                                                                  82;
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                                                                                                 Length 13842;
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US-09-320-878-19

WS-09-320-878-19

Patent No. 6117659

GENERAL INFORWATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: TANG, Li
ITILE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120

CURRENT FILING DATE: 1990-05-27

EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247

EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-09-02
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/110,880
EARLIER FILING DATE: 1998-09-22
EARLIER APPLICATION NUMBER: 60/087,080
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LENGTH: 36778
TYPE: DNA
ORGANISM: Streptomyces venezuelae
US-09-105-537-5
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US-09-105-537-5
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: F88tSEQ for Windows Version 3.0
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Best Local Similarity
Matches 87; Conserv
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51.5%;
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Pred. No. 18;
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APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
FILE REFERENCE: 300622002100
CURRENT APPLICATION NUMBER: US/09/141,908
CURRENT FILING DATE: 1998-08-08
CURRENT FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER APPLICATION NUMBER: PROV. 60/087,080
EARLIER FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: PROV. 60/087,080
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US-09-141-908-1
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; ORGANISM: Streptomyces venezuelae
US-09-141-908-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 38506
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                                                                                                                                                                                                                                                                                    Query Match 2.4%; Score 37.8; Best Local Similarity 51.5%; Pred. No. 18 Matches 87; Conservative 0; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                 440 GGGGAGCTGTTTTGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAGTCTG
                                                                                                                                       500 CATGGGCGTCTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGG
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                                                                                                                                                                                           GCGCGGCCGGCTCATGCAGGAGCTGCCCGCCGGTGGCGCGATGCTCGCCGTCCAGGCCGC 9833
                                           ceeegaecrcarcrecrereacecreccreeeccrrecaccreecc 608
                                                                                            GGAGGACGAGATCCGCGTGTGGCTGGAGACGGAGGAGCGGTACGCGGGACGTCTGGACGT
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CGCCGCCGTCAACGGCCCCGAGGCCGCCGTCCTGTCCGGCGACGCGGAC
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ilarity 51.5%; Pred. No. 18;
Conservative 0; Mismatches
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Sequence 1, Application US/09305640B
Patent No. 6255468
Patent No. 6255468
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham plc
TITLE OF INVENTION: No. 6255468e1 Compounds
FILE REFERENCE: GP30124
CURRENT APPLICATION NUMBER: US/09/305,640B
CURRENT FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2560
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US-09-657-440-19
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US-09-305-640-1/c
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; ORGANISM: Streptomyces venezuelae
US-09-657-440-19
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Patent No. 6509455
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 19
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                                                                                                                                                                                                                                                                                                        Matches 118;
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Me
APPLICANT: BETLACH, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 300622002120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: CIP OF 09/141,908 PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 38506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9834 GGAGGACGAGATCCGCGTGTGGCTGGAGACGGAGGAGCGGTACGCGGGACGTCTGGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9774 GCGCGGCCGGCTCATGCAGGAGCTGCCCGCCGGTGGCGCGATGCTCGCCGTCCAGGCCGC
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                                                                          514 CGGGACAGGCCGCCGCCGGCCGACCGGGCCCAGGTACTTGAGGGCCAGCATAGCCG
                                                                                                                                                                                                                          397 CAGGGCAGAGACTGGGGAGTTCAGGTACCCAGAGATGCTGCTGGGGGGAGCTGTTTTGGGA
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BETLACH, Mary C.
BCDANIEL, Robert
TANG, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCGCCGTCAACGGCCCCGAGGCCGCCGTCCTGTCCGGCGACGCGGAC 9942
CCAGAATGGCGCAGAGGCCGGCGAACACCAGCCCCGACAGCAGGCACACCTCGCGCC
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                                                                                                                                                                                                                                                                                            Score 37.6; DB 3;
Pred. No. 8.3;
0; Mismatches 134;
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Patent No. 6725730
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 119
LENGTH: 2868
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                    Matches 118;
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior Application removed - NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                    Local Similarity
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254
                                                             AGCCCGGGGGCAGGGAGGCCCCGCGCGCGCCCCCCGCGCAGCGGCTCACGTACTTGA 255
                                                                                                                            GGTTCCAGCGCGGCAGCCGGACCGGGCCCCGGTGACGCTGCGCCCAACGGGA
                                                                                                                                                                                         AGCCCGGGGGGAGGCCCCGCGCGCGCCCCCGCGCAGCGGCTCACGTACTTGA 275
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                                                                                         GTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCC 636
                                                                                                                                                        TGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGAGCTCATCTGCT
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Gurney, Austin L.
Sherwood, Steven
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                             CCAGTGGGACCT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood, William
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Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart, Timothy A.
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Pred. No. 8.6;
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RESULT 86 US-09-774-528-383/c

383, Application US/09774528 5. 6743619

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; LOCATION: (92)..(1309)
US-09-774-528-383
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CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt FL genes Version 2.0
SEQ ID NO 383
                                                                                                                                                                                                                                                                                                              Sequence 9715, Application US/09252991A Patent No. 6551795
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Best Local Similarity 50.9%;
Matches 89; Conservative
                                                         SEQ ID NO 9715
                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                 APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR EILING DATE: 1998-02-18
                                                                            PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: No. 6743619el Nucleic
TITLE OF INVENTION: Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
ORGANISM: Pseudomonas aeruginosa
                                       ENGTH: 648
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Zhou, Ping
Zhou, Ryle
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Wang, Dunrui
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Wehrman, Tom
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di, Vinod
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Pred. No. 8.1;
O; Mismatches 86;
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Patent No.
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Best Local Similarity
                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
PILING DATE: 28-APR-1993
PRIOR APPLICATION NUMBER: 92.401.231.3
APPLICATION NUMBER: 92.401.231.3
APPLICATION NUMBER: 92.401.231.3
APPLICATION NUMBER: 93.401.231.3
APPLICATION NUMBER: 19.683
RESERRENCE/DOCKET NUMBER: 410.007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                         TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2150 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEIVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY O
TITLE OF INVENTION: IMMUNOLOGY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                TELECOMMUNICATION INFORMATION: (212) 661-8000
            TYPE: nucleic acid
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STRANDEDNESS:
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Pred. No. 6.5;
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RESULT 89
US-09-428-711A-13/c
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                                                                                                                                                                                             SOFTWARE: Fas
SEQ ID NO 13
LENGTH: 3995
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09428711A Patent No. 6358720
 Query Match
Best Local Similarity
Matches 117; Conserv
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APPLICANT:
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                                                            LOCATION: (1)...(3995)
OTHER INFORMATION: n = A,T,C
-09-428-711A-13
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PRIOR FILING DATE: 1997-04-20
NUMBER OF SEQ ID NOS: 21
PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/428,711A CURRENT FILING DATE: 1999-10-28 PRIOR APPLICATION NUMBER: PCT/JP98/01246 PRIOR FILING DATE: 1998-03-23
                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP : PRIOR FILING DATE: 1997-04-28
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shirasawa, Takuji
APPLICANT: Tokumitsu, Hiroshi
APPLICANT: No. 6358720uchi, Teruhisa
TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE
FILE REFERENCE: 06501-045001
                                                                                              NAME/KEY: CDS
LOCATION: (388)...(3540)
NAME/KEY: misc_feature
                                                                                                                                                               TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                      FEATURE:
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HYPOTHETICAL: I
ANTI-SENSE: NO
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ORGANISM: Huma
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NAME/KEY:
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 2.4%;
ilarity 46.2%;
Conservative
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   0;
Score 37.2; DB 3;
Pred. No. 12;
0; Mismatches 136;
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                             Length 3995;
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RESULT 91
US-09-839-479-28
; Sequence 28, Application US/09839479
; Patent No. 6727222
; Patent No. 6727272
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US-09-418-710-28
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; LOCATION: (346)...(4926)
US-09-418-710-28
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CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
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TYPE: DNA
ORGANISM: Homo
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Patent No. 6596482
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                                                                                                                                                                                                                                                                                                                                      Query Match 2.4%;
Best Local Similarity 53.4%;
Matches 78; Conservative
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TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                   4028
                                                                                                                                                                                                                                                                  3908 AAGTTTGTCCAAAGAAAGGTGAGGATGACAAATTGATCTTGTGTGATGAGTGTAATAAAG
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                                                                                                                   GCCCAGCTTGCCAGCCCGCTACTGCC
                                                                                                                                                     GCTCCAGCTGCCTGCAGGCAACAGTC
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Pred. No. 13;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: JONES, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002

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                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (346)...(4938)
US-09-418-710-30
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LENGTH: 5561
                                                                                                                                                                                                                                                            SEQ ID NO 30
LENGTH: 5573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30, Application US/09418710 Patent No. 6596482
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Best Local (
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CURRENT FILLING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo:
                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9
PRIOR FILING DATE: 1997-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042001
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
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CURRENT FILING DATE: 2001-04-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 9/116570
                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: NAME/KEY: CDS
LOCATION: (346)...(4926)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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3920 AAGTTTGTCCAAAGAAAGGTGAGGATGACAAATTGATCTTGTGTGATGAGTGTAATAAAG 3979
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                                  535 ACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCGGG 594
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                                                                                           Similarity
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                                                                       Conservative
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                                                                                                                                                                                                                                                                                                   for Windows Version 4.0
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                                                                                         2.4%;
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                                                                       Score 37.2; D
Pred. No. 13;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.2;
Pred. No. 1:
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                                                                                                          Length 5573;
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US-09-839-479-30
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                                                                                                                                                                                                                                                 Sequence 1, Application US/08146930 Patent No. 5958764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 30
LENGTH: 5573
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Roop, Do
APPLICANT: Rothmago
APPLICANT: Greenha
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Best Local Similarity
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Patent No. 6727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
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TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: NAME/KEY: CDS
LOCATION: (346)...(4938)
                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                        TITLE OF INVENTION:
                              CITY: Los Angeles
STATE: California
                                                                     STREET:
               COUNTRY:
                                                                                      ADDRESSEE:
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90017
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                                                                  611 West Sixth
                                                                                                                                                         Rothnagel, Joseph A.
Greenhalgh, David A.
WENTION: SPECIFIC EXPRESSION VECTORS
               U.S.A.
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                                                                                   TAON & TAON
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                                                                                                                                          AND METHODS OF
                                                                     Street
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Pred. No. 13;
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RESULT 95
US-08-458-240-1/c
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                                                                                                                                                  Sequence 1, Application US/08458240 Patent No. 6143727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
GENERAL INFORMATION:

APPLICANT: Roop, Dennis R.

APPLICANT: Rothasgel, Joseph A.

APPLICANT: Greenhalgh, David A.

TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS

TITLE OF INVENTION: AND METHODS OF USE

NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 6530 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 07/876,286
FILING DATE: Appril 30, 1992
APPLICATION NUMBER: No. 5958764 yet assigned (204/132)
FILING DATE: October 29, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600 TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IEM PC compatible
OPERATING SYSTEM: IBM MS-DOS (Vergion 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                3197
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                                                                                                                                                                                                                                                                                                                     GGCCCTGCACCC 892
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Pred. No. 14;
0; Mismatches 153;
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RESULT 96
PCT-US93-03993-1/c
; Sequence 1, Application PC/TUS9303993;
; GENERAL INFORMATION:
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Best Local Similarity 47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordDerfect (Version 5.1)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER: 07/876,286
FILING DATE: April 30, 1992
APPLICATION NUMBER: No. 6143727 yet assigned (204/132)
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Pred. No. 14
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vf

CURRENT APPLICATION DATA:
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NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
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INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL:
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LENGTH: 6530 base pairs
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
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APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: CONSTITUTIVE AND INDUCIBLE EPIDERMAL
TITLE OF INVENTION: VECTOR SYSTEMS
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Pred. No. 1
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Best Local S
Matches 184
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GENERAL INFORMATION:
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COMPUTER READABLE Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATECRITIN Release #1.0, 1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/183,861
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INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE:
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LENGTH: 516 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
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APPLICANT: Campos-Neto,
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANI
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CLASSIFICATION:
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CÉCGTGÉCTCCAGCTCGGCGCGCTGCTGCGTGGCGGTGTCTAGGCGCGCTGCTGCAGCTCCT
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                                                                    CCTCGGCGTTCGCGGCCAGCTGCTGGCGGGCCTCGTCGCCGTCCGCGGCCAGCCGTGCCA
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Pred. No.
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US-09-022-765-34/c
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Patent No. 6
                                                                                                                                                                                                                                                                                                      Matches 184;
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 35
SEQUENCE CHARACTERISTICS:
LENGTH: 516 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Reed, Steven
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ORIGINAL SOURCE:
ORGANISM: Lei:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANI
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
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CTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCGCTGCCACCTTCCCAGCCGGCACC 1034
                                 CCACCTGTGCCTCCAGCTCGGCGCGCTGCTGCTGCGGGGGGTGTCTAGGCGCTGCTGCAGCT
                                                                TCAGCAGAACCT - GCCTCCTGGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTG
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TYPE: DNA
; ORGANISM: Leishmania major
US-09-551-974A-34
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; SEQ ID NO 34
; SEQ ID NO 34
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Patent No. 6
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/551,974A
CURRENT FLING DATE: 2000-04-14
CURRENT FLING DATE: 101
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Skeiky, Yasir A.W.
NVENTION: LEISHMANIA ANTIGENS FOR USE IN
NVENTION: THERAPY AND DIAGNOSIS OF LEISHW
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CGGCGTTCGCGGCCAGCTGCTGGCGCGCCTCGTCGCGGTCCGCGGCCAGCC
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                                                                CCCGTGCCTCCAGCTCGGCGCGCTGCTGCTGCGTGGCGGTGTCTAGGCGCTGCTGCAGCTCCT
                                                                                              TCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCT
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RESULT 100
US-09-565-501A-34/c
; Sequence 34, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:

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APPLICANT: Reed, Steven G.

APPLICANT: Webb, John R.

APPLICANT: Webb, John R.

APPLICANT: Dillion, Davin C.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Shatia, Ajay

APPLICANT: Shatia, Ajay

APPLICANT: Bhatia, Ajay

APPLICANT: Peter Probst

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS

FILE REFERENCE: 210121.420C6

CURRENT APPLICATION NUMBER: US/09/565,501A

CURRENT FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 112

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 516

TYPE: DNA

ORGANISM: Leishmania major

US-09-565-501A-34
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Search completed: February Job time : 195 secs
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Best Local Similarity 44.8%;
Matches 184; Conservative
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/tissue_type="pooled germ cell tumors"
/lab host="DH10B"
/clone lib="NCI CGAP GC4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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1 (bases 1 to 1506)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera; S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM6928"
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VERSION KEYWORDS SOURCE ORGANISM

Homo

sapiens (human) sapiens

RESULT 2 AY419550

DEFINITION ACCESSION

AY419550

1506 bp VIRTUAL

TRANSCRIPT,

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875

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1038 815 918

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Homo sapiens AIRE gene, l genomic survey sequence. AY419550 AY419550.1 GI:39775507 GSS.

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ORIGIN

Query Match Best Local Simi Matches 624;

Similarity

39.6%;

Conservative

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Score 612.4; DB 5; Pred. No. 1.3e-127; 0; Mismatches 1;

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ACCESSION
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                           Rockville, MD 20850, USA
These sequences were made by
them based on alignment.
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GSS.
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Pan troglodytes AIRE gene, VIRTUAL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM6928"
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JOURNAL COMMENT REFERENCE AUTHORS SOURCE ORGANISM RESULT 4 AA742555/c LOCUS KEYWORDS VERSION ACCESSION DEFINITION TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 433) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. found through the I.M.A.G.E. Consortium/LLNL www-bio.llni.gov/bbrp/image/image.html Insert Length: 701 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, Tumor Gene Index Unpublished (1997) Homo sapiens mRNA sequence. nx30cll.sl NCI\_CGAP\_GC4 Emmert-Buck, M.D., Ph.D. Contact: Robert Strausberg, Ph.D. Homo sapiens AA742555.1 AA742555 cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be GI:2782137 (human) Homo 433 bp mRNA linear EST 22-JAN sapiens cDNA clone IMAGE:1257620 Hominidae; M.D., Project Ph Euteleostomi; EST 22-JAN-1998 (CGAP), Michael эd

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RESULT 5
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                                     AUTHORS
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
                                                                                                                MUB
                                                                                                                               genomic survey sequence.
AY419552
AY419552.1 GI:39775509
GSS.
                                                                                                                                                                                            AY419552
Mus musculus AIRE gene,
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                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                   Mua muaculua
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                                                (bases 1 to 1512)
                                                                                                                musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Glone lib="NCI CGAP GC4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1257620"
/tissue_type="pooled germ
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 6.8e-74;
                                                                                                                                                                                              1512 bp
VIRTUAL
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                                                                                                                                                                                               sequence,
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Best Local S
Matches 414
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JOURNAL
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rockville, MD 20850, USA
These sequences were made by
them based on alignment.
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Science 302 (5652), 1960-1963 (2003)
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Inferring nonneutral evolution from human-chimp-mouse
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                    CGCCGCTGCCTTCCACTGGCGCTGCCACTTCCCCAGCCGGCACCTCCCCGGCCCCGGGACGGG
                                                                                                                                                                                                                                                                                                          CACGACTCTTGTCTACAAGCACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Pred. No. 3.2e-53;
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RESULT 6
BE627856
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AUTHORS
TITLE
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ORGANISM
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61
                                                             Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1977)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available additionable for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE627856
451 bp mRNA linear EST 24-AUG-200 uu49c07.y1 Soares_thymus_2NDMT Mus musculus cDNA clone IMAGE:3375276 5' similar to TR:Q9Z0E3 Q9Z0E3 AIRE PROTEIN. ;, mRNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 451)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus
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                                                                                                                                            Similarity
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                                                             GIGIGGCGATGCCACGGTGTTGCGGTGTGCACACTGTGCCGCTGCCTTCCACTGGCG
                                                                                       GTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTTCCACTGGCG
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                  CTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: :
Location/Qualifiers
                                                                                                                             Conservative
                                                                                                                                                                                                                         Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:3375276"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
                                                                                                                                            10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _type="mRNA"
                                                                                                                             <u>0</u>
                                                                                                                         Score 162.6; DB 2
Pred. No. 5.5e-26;
0; Mismatches 84
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                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                NS. Okazaki, Y., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinoich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wanner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yang, I., Yang, L., Xawai, J., Aizawa, K., Yang, L., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y., Sasaki, K., Sasaki, D., Shibata, K., Shimadai, K., Sasaki, K., Sasaki, D., Shibata, K., Shimasi, Y., Sasaki, Y., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDMAs
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BY728790 RIKEN full-length enriched,
clone C330016003 5', mRNA sequence.
                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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BY728790.1
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
                                                                                                     Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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l, ES cells Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohseto, N., Saito, R., Sakazume, N. Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Genome Sequences Mamm.
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                                                                                                                                                                                                                                                                                                                                                                 GGGAGCTCATCTGCTGACGGCTGCCCTCGGGCCTTCCACCTGGCCTGCCCTGTCCCCTC
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ACCAATCTCCGCTT-GCAATCCTGCTGCAGACTCGACTCCCACGCCAGGCACACCGGG
                                                TCCCCCCGGGGCTTAGGTCGGCGGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCTAG
                                                                                                      AACAGAACCTGTCCCAGCCTGAGGTGTCCAGGCCCCCGGAGCTACCTGCAGAGACCCCGG
                                                                                                                                                            AGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCGGCCCCAGGAGCCACCCCGTGGAGACCCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="RIKEN full-length enriched, ES cells"
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | type="ES cells"
|host="SOLR"
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Pred. No. 1.6e-24;
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Klausner, R.D., Colline, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkine, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W.,
Villalon, D. K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Villalon, D. K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Villalon, D. K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettenan, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
DNA sequences
12,477a23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 CGAAGCTGTACNCACCTCTGGGCCCCGTCCAGCACCTGGGCTTGCC 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (24-MAR-2004) National Institutes of Health, Mammalian Submitted (24-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                             Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at http://image.llnl.gov Series: IRAK Plate: 138 Row: g Column: 15 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Prescherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schmerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
Tissue Procurement: Marcello Bento Soares, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus
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                                                                   Location/Qualifiers
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musculus'
                                                                                                                                                                                                                                                                                     Holt, Marco Marra.
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frame-shift
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REFERENCE
AUTHORS
TITLE
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Matches 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           706
                                                                                                                                                                                                                                                                                                       Other_ESTs: uu49c07.yl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE630816 511 bp mRNA linear EST 25-AUG-200 uu49c07.x1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:3375276 3' Similar to TR:Q9Z0E3 Q9Z0E3 AIRE PROTEIN. ;, mENA
                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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EST.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                             MGI:1084880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAACGAGGATGAGTGTGCCGTGTGCCACGACGGAGGTGAGCTCATCTGTTGTGACGGCT
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                                                                                                                                                                                                                                                          quality sequence stop: 391.
Location/Qualifiers
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/tissue_type="Thymus gland, mous
/clone_lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1282549"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Vector: pT7T3-Pac"
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                                                                                                             tissue_type="Thymus"
dev_stage="4 weeks"
                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:3375276"
                                                                                                                                                                                             mol_type="mRNA"
|strain="C57BL/6J"
                                                                                                                                                sex="male"
                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.7%;
    double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                host="DH10B"
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Pred. No. 6e-23;
0; Mismatches
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA866922 542 bp mRNA linear EST 16-
vx91b07.r1 Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:1282549 5' Similar to TR:015164 015164 TRANSCRIPTION
INTERMEDIARY FACTOR 1. ;, mRNA sequence.
                                                                                                                         Seq primer: -28m13 rev2 ET from High quality sequence stop: 472. Location/Qualifiers
                                                                                                                                                                                                                                   MGI:674349
                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                  WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
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AA866822.1
                                                                                                                                                                                                           Possible reversed clone: similarity on wrong strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Pharmacia), digested with Not I and cloned into the Nand Eco RI sites of the modified pTTT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:2962267
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Pred. No. 2.1e-14;
0; Mismatches 77
                                                                                                                                                                                      Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77;
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Length 420; Indels

6,

Gaps

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SM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 420)

Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,

Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,

Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,

Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,

Payne,R., Potter,D.G., Qiann,N., Schrick,J., Shi,Z.-Z.,

Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Malke,W., Xu,N.,

Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Malke,W., Xu,N.,

Zhu,Q., Person,C. and Sands,A.T.

Zhu,Q., Person,C. and Sonds,A.T.

Wankl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention

L. Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                             Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence. CG513175 CG513175.1 GI:37299748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG513175 420 bp
OST66421 Mus musculus 129Sv/Ev I
                                                                                                                                                                                                                                          Lexicon Genetics Incorporated 4000 Research Forest Drive, Temail: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                        Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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/clone="OST66421"
                                                             /mol_type="genomic DNA"
/strain="129Sv/Ev"
                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
cell_type="embryonic stem cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                   . .420
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83.2%;
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Pred. No. 6.9e-10;
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TITLE
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ORGANISM
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VERSION
KEYWORDS
ORIGIN
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AI552580/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1143 GCCAA-----GGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 384)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI552580 384 bp mRN vx26b07.x1 Soares_mammary_gland_NbMMG IMAGE:1265557 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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AI552580.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone was previously sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:668109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCCTCCTCAATGAGCACTCATTTGACGGCATCCTGCAGTGGGCCATCCAGAGCATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCCTTCTGAGCGAGCACCTTCGATGGCATCCTGCAGTGGGCCATCCAGAGCATGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is from the 3' end quality sequence stop: 381. Location/Qualifiers
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                                   T 3']; double-stranded cDNA was ligated to Bco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                           /clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary gland; VecTor: pT73D-Pac
/pharmacia, with a modified polylinker; Site_1: Not I.
Site_2: Eco RI; 1st_strand cDNA was primed with a Not
                                                                                                                                                   /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:1265557"
                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                           sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:4484943
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Pred. No. 1.2e-09;
0; Mismatches 58
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musculus
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EST 23-MAR-1999 CDNA clone

202 1256 142 1196 82 1142 1,

RESULT 11 CG513175

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ORIGIN

Query Match Best Local S Matches 104

104;

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TCTGG

646 478 586 418

CCTGG

REFERENCE AUTHORS

SOURCE

ORGANISM

KEYWORDS ACCESSION DEFINITION

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ACCESSION
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AG069825
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666 CTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCAGGAGCCA
                                                                             136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC encess generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: F
AG069825 AG069825.1 GI:16621627
GSS.
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Totoki, Y., Watanabe, H. a.
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:9598"
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Pred. No. 8.5e-06;
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0; Mismatches 30
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AL241809.1 GI:7962578
ASS; genome survey sequence.
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Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
Roest Crollius,H., Jaillon,O., Dasilva,C., Boune Bernot,A., Fizames,C., Wincker,P., Brottler,P., Saurin,W. and Weissenbernoth,D. Estimate of human gene number provided by genome using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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022016 of library G from Tetraodon nigroviridis, genom
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                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 925)
                                                                                                                                                                                                                                                               CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of reshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
Submitted (02-JUN-1999) Genoscope
BP 191 91006 EVRY cedex - FRANCE (
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                            fly), genomic survey sequence.
AL053013
AL053013.1 GI:4934461
GSS.
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/note="Genoscope sequence ID : COBG022BH08SP1-end
PUC-Ori"
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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Pred. No. 1.1e-05;
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                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, 1 (bases 1 to 674)
Bonaldo, M. F., Lennon, G. and Soares, M.B.
                      97044477
                                    Genome Res. 6 (9),
                                                         discovery
                                                                                                                                                               Homo sapiens
                                                                      Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two app
                                                                                                                                                                            Homo sapiens (human)
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                                                                                                                                                                                                                GI:23680847
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                              1133 CCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGC 1174
                                                                                                                                                                                                         1013 CTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTC
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CSTYBMBCYTSTSCGGSSSSSGKGGVTKCGCGGCGSSSTNGMBGTSSACSSSSSSSSSSSS
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
|clone="BACR19D16"
|clone="BACR19D16"
|clone_lib="RPCI-98"
|note="end : TET3"
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Pred. No. 6.2e-05;
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                                                                                                                                                                                                                                                                                               GGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCCTGTGCGACACCTGCCCGAGGGCCTACCATCTCGTGTGCCTGGACCCAGAGCTGGA 522
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/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)
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Pred. No. 6.6e-05;
D; Mismatches 72;
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UI-E-EJ0-aii-m-23-0-UI.rl UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-aii-m-23-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 319 335 8250
Fax: 319 335 9565
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375 Newton Road , 4156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coordinated Laboratory
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bento-soares@uiowa.edu
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TTGCCTGTGCCAGAAGAATGAGGACGAGGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCAT 571
                                                                               TGGTCTGTCTCATAGCCGTCAGGATTACTGTGAGGTGTGCCAGCAGGAGGTGGGGAGATCAT
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                            /Clone lib="UI-B-EJO"
//Clone | Torgan: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-B-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CGCCGC; Retina Poveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI.E-EJ0-aii-m-23-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE a
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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Best Local :
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5', mRNA
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   AQ474914 350
CITBI-E1-2591L22.TF CITBI-E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: trop@sanger.ac.uk
Sanger Kenopus tropicals EST project 2001
TROPICALIS SEQUENCE ID: THdA010e06.plkbSP6
This sequence is from a Xenopus Gene Colleconstructed by Nigel Garrett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus; Silurana.

(bases 1 to 940)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers, Sanger Xenopus tropicalis EST project 2001 (2004)
Unpublished (2004)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanger Institute
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                                                                                                                                                                                                                                                        GGCTCCCGAGGGCAAGTGGAGCTGCCCCCACTGTGAGAAGGAGGGGGATCCAGTGGGAGCC
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                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="THdA010e06"
/dev gtage="tailbud head (gtage 28-30)"
/dev gtage="tailbud head (gtage 28-30)"
/lab_nost="WBcherichia coli DH10B."
/clone_lib="XGC-tailbud-head"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from tailbud
head. EcoRI-NotI cut cDNA was then ligated into pCS107
with EcoRI at the 5' end and NotI at the 3' end."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
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Xenopus tropicalis cDNA clone THdA010e06
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Matches 68; Conserv
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Other GSSs: CITBI-E1-2591122.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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AV591350 Bos taurus brain
5', mRNA sequence.
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                                   Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                       Takasuga, A., Hi
and Sugimoto, Y.
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                 Bos taurus (cow)
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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 350)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAGTCCCCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                       GAGCGAGGTAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGGATGACACTGCCAGTCACGAGCCCGCTCTGCACAGGGATGACCTGGAGTCCCTTCT
                                                                                                           (bases 1 to 563)
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     Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="CITBI-E1"
/note="Vector: pBeloBAC11;
Callech Human BAC Library !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DN
/db_xref="taxon:9606"
/clone="2591L22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'sex="male"
                                                                                                                                                                                                                                        GI:9702343
                                                                                        Hirotsune, S., Itoh, R., Jitohzono, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.2%;
     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65.6; DB 8;
Pred. No. 0.00044;
0; Mismatches 4
   (22), E108 (2001)
                                                                                                                                                                                                                                                                                                              563 bp
                                                                                                                                                                                                                                                                                             fetus
                                                                                                                                                                                                                                                                                             Вов
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Site_1:
                                                                                                                                                                                                                                                                                             taurus cDNA clone E1BR018A07
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REFERENCE
AUTHORS
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PUBMED
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Best Local
                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACCGCTGCCCTCG
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Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21570554
11713328
                                                                                                                              Analysis of bovine mammary gland EST the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                              1 (bases 1 to 610)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing.
This clone was obtained from a Location/Qualifiers
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                    BE590137.1 GI:9843176
EST.
                                                                                                                                                                                                                                                                                                                                                                                  610 bp
197111 BARC 5BOV Bos taurus cDNA
Email: tads@lpsi.barc.usda.gov
                                              USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                               Contact: Sonstegard TS
                                                                                                                                                                                  and Quackenbush,J.
                                                                                                                                                                                                                                                                                                    Bos taurus
                                                                                                                                                                                                                                                                                                                  Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-248-25-5725
                                                                                                  12140684
                                                                                                                                                                                                                                                    Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCTACCACATCCACTGTCTGAACCCCCCCCCCCGACATCCCCCAACGGCGAATGGCT
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               301 504 8416
301 504 8414
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/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="E1BR018A07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
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56.2%;
                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Pred. No. 0.00064;
0; Mismatches 95
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5', mRNA sequence.
                                                                                                                                                                 and functional annotation of
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Matches 101;
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                                                                                               National Cancer Institute / NIH
Bldg. 31 RmL0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Wei WU / Prof. Christof NIEHRS
cDNA Library Preparation: Wei Wu, DKFZ
cDNA Library Preparation: Wei Wu, DKFZ
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM14930 row: k column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587 bp mRNA linear EST 14 AGENCOURT 21860720 XtSt10-30 Xenopus tropicalis cDNA clone IMAGE:7092432 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus tropicalis
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Location/Qualifiers
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 117 row: I column: 4
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PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus tropicalis (western clawed frog
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                              quality sequence stop: 587.
Location/Qualifiers
1. .587
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/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/ibrary made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and dises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
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organism="Xenopus tropicalis"
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Pred. No. 0.00064;
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BP 191 91006 EVRY CRUEA.

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton project grant are Pavan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL106054
AL106054.1 GI:5619805
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS015Y4 linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGATCTGCACCTTTTGCCGGGACCTGTCCAGACCAGAAGTGGAG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAAAGTTTTCCACCTGTCGTGCCACGTGCCTACACTGATGAACTTTCCCAGTGGTGAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCCAGTGGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATGAGGACTGGTGTGCTGTATGTCAGAATGGGGGGGAGCTGCTTTGCTGTGAAAAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATGAGGACGAGTGTGCCGTGTCGGGACGCCGGGGAGCTCATCTGCTGTGACGGCTGC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="MAGB:7092432"
/clone="MAGB:7092432"
/clone=Tib="whole embryo, pool of stages 10, 20 and 30"
/tissue type="whole embryo, pool of stages 10, 20 and 30"
/clone_Tib="xtst10-30"
/note="Vector: pRKW2; Site 1: BamHI; Site 2: XhoI; 10 ug
/note="Vector: pRKW2; Site 1: BamHI; Site 2: XhoI; 10 ug
/note="Vector: pRKW2; Site 1: BamHI; Site 2: XhoI; 10 ug
/note="Vector: pRKW2; Site 1: BamHI; Site 2: XhoI; 10 ug
/note="Vector: pRKW2; Site 1: BamHI; Site 2: XhoI; 10 ug
/note="Vector: pRKW2; Site 1: BamHI; Site 2: XhoI; 10 ug
/note="Vector And 30 and primed by oligo-dT primer:
5'-GAGAGAGAGC(T)16VN-3' (where V=G,A,C)

5'-GAGAGAGAGAGCACT(CCGAGTTAATTAATC)

111-length enrichment, oligo-dG tailing and normalization
against itself, second-strand synthesis was carried out by
priming with 5'-GAGAGAGAGCTCGAGTTAATTAAT(C):3-3' dabNA
was digested with XhoI/BamHI and directionally cloned into
the pRKW2 vector. Average insert size is 1.5 kb. Library
constructed using the Carninci protocol (Genome Research
2000) by Drs. Wu and C. Niehrs (DKFZ, Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence.
/organism="Drosophila my/organism="Drosophila my/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15E10"
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.2%;
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Pred. No. 0.00097;
0; Mismatches 63;
                                                                       melanogaster"
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KEYWORDS
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CK704772/c
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Best Local S
Matches 166
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

E 1 (bases 1 to 807)

E Wei.C., Mathavan.S., Thoreau,H., Lim.L., Lee,C. and Ruan
Genome Institute of Singapore, Zebrafish Gene Collection
Unpublished (2004)

Contact: Ruan Y

Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 GGGACCTGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCCGGGCA
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               Email: ruanyj@gis.a-star.edu.sg
GIS Clone ID: ZF101-P00008-BR2_E20
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK704772 807 bp r
ZF101-P00008-DEPE-R E20 GISZF001_ra
IMAGE:7137214 3', mRNA sequence.
                                                                                           Tel: +65 6478 8073
Fax: +65 6478 9059
                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CK704772.1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCGCCTGGCCCTGGCCTGCC
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/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:42480721
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                                                                                                                                                                                                                                                                Lee, C. and Ruan, Y. Gene Collection
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1121 1096 1061 1036 1001 976 941 916 881 856 821 796 761 736 701

REFERENCE AUTHORS TITLE JOURNAL

Euteleostomi;

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EST 30-MAR-2004 A clone

COMMENT

FEATURES

source

SOURCE ORGANISM

VERSION ACCESSION **ŒYWORDS** 

RESULT 23 CNS015Y4

DEFINITION

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238

178

Query Match Best Local S Matches 102

102;

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AG030591
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Best Local Similarity
      AUTHORS
                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 GAAGAATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGG
                                                                                                                                                                                                                                                                                                                        Pan troglodytes DNA, clone: PTB-003A10.F, genomic AG030591
AG030591.1 GI:16557464
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC
                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                    Pan troglodytes (chimpanzee)
Pan troglodytes
Fujiyama, A., Hattori, M.,
                                                          Unpublished
                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             creccrceeeccrrccaccreeccreccreccrccecrcceeeaaaarccccaeree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATCATCAGGATTACTGTGAGGTCTGCCAGCAGGAGGAGAGATCATTCTCTGTGACAC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTCCACGGGCCTATCACATGGTCTGCTTGGACCCCGACATGGAGAAGGCCCCTGAGGG
                           (bases 1 to 888)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linker/adaptor sequence: same as the priming sequence; Average insert size: 2kb; For PCR insert analysis: Use M13 Forward and reverse primers; Library Amplified; Recombinants (inserts): 98%; Library complexity: 5x106; Full-length construction (method): SMART, a Clontech method The pooled tissue RNA was collected and used to construct full length enriched cDNA library and also served as template to synthesize complex first strand cDNA probe. Two high density colony arrays were made from over intensity clones and hybridized with the probes. Low intensity clones were selected as they represented rare expressed clones. The hybridization intensities for all clones span from 0 to 1.8 million counts and the low abundant class ranged from 0 to 13,000."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.ATTCTÁGAGGCGÁGGCGÁCCATG(T)30VN ; Directionally cloned, 5 cloning site: Sfi A site GGCCATACGGCC ; linker/adaptor sequence: 5.AACCAGTGGTATCAACGCAGAGTGGCC ; 3' cloning site: Sfi B site GGCCGAGGCGGC; 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Site
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/note="Vector: pDNR-LIB, Site_1: Sfi A (GGCCATTACGGCC);
/note="Vector: pDNR-LIB, Site_2: Sfi B (GGCCGAGGGGGGCC); Priming method: Sfi-(dr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Embryo"
/dev_stage="7 Different embryonic Stages(From just
/fertilized Embryos to 72 hours just hatched baby fish)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Singapore local strain"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE:7137214"
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                                                                                                                                                                                                      Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Toyoda, A., Taylor, T.D., Yada, T.,
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Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(R-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9171)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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R.Site 2 : SacI.
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/clone_lib="PTB_Chimpanzee_Male_BAC_Library"
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/db_xref="taxon:9598"
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Pred. No. 0.0014;
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Best Local Similarity
Matches 100; Conserv
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vn94e11.rl Stratagene mouse heart
IMAGE:1039628 5', mRNA sequence.
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Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Sequence cleaned of vector, adaptator and repetitions. Contact us

at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003)
Contact: Tosser-Klopp G
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EST.
Sus scrofa (pig)
Sus scrofa
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Chemin de Borde-Rouge - Auzeville
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1 (bases 1 to 783)
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/db_xref="taxon:9823"
/db_xref="taxon:9823"
/clone="scan0028d.a.12"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/dev_stage="from embryos to adults"
/clone_lib="Sus Scrofa library (scan)"
/note="cissues: adipose tissue, brain, kidney, liver,
/muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
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/mol_type="mRNA"
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61.78;
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Pred. No. 0.0015;
0; Mismatches 62;
                                  mRNA linear EST 09-FEB-1998 (#937316) Mus musculus cDNA clone
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Best Local S
Matches 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                               340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 TTCCTACCACATCCACTGCCTGAACCCCCCGCTGCCAGAGATCCCAAACGGCGAATGGCT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 GGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATCCCCCAGTGGGACCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 GGACGAGTGTGCCGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                    CF161888
CF161888.1
EST.
                                                                                                                                                                    CP161888 485 bp mRNA linear ES B0703E06-5 NIA Mouse Embryonic Germ Cell cDNA Library musculus cDNA clone NIA:B0703E06 IMAGE:30458165 5', mF
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89;
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4444 Forest Park Parkway, Box 8501, St. Lo
Mus musculus
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 403.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
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EST.
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/dey stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/clone_lib="Stratagene mouse heart (#937316)"
/clone_Torgan: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/clone_Torgan: heart; Vector: pBluescript SK-; Site_1:
/clone_Torgan: heart; Vector: primer:
/clone_Torgan: heart; Vector: primer:
/clone_Torgan: heart; Vector: primer:
/clone_Torgan: heart; Vector: pBluescript SK-; Site_1:
/clone_Tor
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/strain="NIH Swiss"
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/clone="IMAGE:1039628"
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                                  (house mouse
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Pred. No. 0.0016;
0; Mismatches 43;
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Best Local (
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                                    593 GGCCTTCCACCTGGCCTGCCTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAG
115 TTCCTACCACATCCACTGCCTGAACCCCCCCGCTGCCAGAGATCCCAAACGGCGAATGGCT 174
                                                                                                                                                                                                                                                    89;
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National Institutes of Health
National Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0703 row: E column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 485)
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                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG
                                                                                                                   GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGAGCTCCTGTGCTGTGACACATGCCCTTC 114
                                                                                                                                                                                                                                                Conservative
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/note="vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
/note="vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
/note="vector: pCMV-SPORT6 (Invitrogen); Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). (PMID: 11544199)). Total
RNAs were obtained from Dr.Mark G. Carter (NIH/NIA-IRP).
EG cells were cultured at 37. C, 5% CO2 in DMEM
supplemented with 15% ES cell-qualified FBS, 0.1mM
non-essential amino acids, 2 mM golutamine,
penicallin/strepcomycin, 1 mM sodium pyruvate, 0.1 mM
beta-mercaptoethanol, and 10000000 units of LIP per liter.
Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                              2.5 up of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 4.0 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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(Long)"
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/lab_host="DH10B"
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/strain="C57BL/6J"
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Pred. No. 0.0016;
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                                                                                                                                                                                                                                                                                                        Length 485;
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: B0181 row: H column: 02 Seg primer: -21M13 Reverse High quality sequence aron. E74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA893864 514 bp mRNA
B0181H02-5N NIA Mouse Neural Stem Cell (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library (Long)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 514)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Ko,M.S.H.
Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Aiba, K., Vescovi, A.L
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      CDNA Library (Long)
                                                                                                                                                                                                                                                                                                                                                                                               /clone="NIA:B0181H02 IMAGE:30101653"
/dev_stage="Adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="NIA Mouse Neural Stem Cell (Differentiated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="niaEST:B0181H02-5N'
                                                                                                                                                                                                                                                                                                                                                                                                                                             xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Мив.
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Query Match Best Local Similarity

4.18;

Score 63.2; DB 6; Pred. No. 0.0016;

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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: K0332 row: G column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 562)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Umezawa,A. and Ko,M.S.H.
Umezawa,A. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA564994
CA564994.1 GI:25109673
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Other_ESTs: K0332G02-3
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA564994 562 bp mRNA linear EST 19-NOV-200
K0332602-5N NIA Mouse Osteoblast cDNA Library (Long) Mus musculus
CDNA Clone NIA:K0332G02 IMAGE:30057385 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGGGGGCTCCTGTGCTGTGACACATGCCCTTC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (house mouse)
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/clone lib="WIA Mouse Obteoblast cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2:
Not1; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Dr. Akihiro Umezawa (Keio University School
of Medicine, Japan). Double-stranded cDNAs were
synthesized with an Ollgo(dT) primer (Invitrogen:
5'-pGACTAGGTCGGCGCCCCTTTTTTTTTTTTTT-3') from
2.1 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lone-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
products were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sall and NotI enzymes
and cloned into Sall/NotI site of pSPORT1 plasmid vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="NIA:K0332G02 IMAGE:30057385"
/tissue_type="Osteoblast"
/cell_line="KUSA-A1 cells"
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Matches Query Match Local 193 653 GTGCTCCAGCTG 664 133 TTCCTACCACATCCACTGCCTGAACCCCCCGCTGCCAGAGATCCCAAACGGCGAATGGCT 593 GGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGAG 533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592 Similarity CTGTCCCCGCTG 204 GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGGAGCTCCTGTGCTGTGACACATGCCCTTC Conservative The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao (NIA)." 4.1%; o ; Score .63.2; DB 6 Pred. No. 0.0016; Mismatches 6, 43; Length Indels <u>.</u> 652 132 192

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REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 31 BB654405 LOCUS SOURCE ORGANISM DEFINITION Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 564)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001) Contact: Yoshihide Hayashizaki BB654405 RIKEN full-length enriched, 2 days neonate thymus thymic cells Mus musculus cDNA clone C920008E20 5', mRNA sequence. Mus musculus BB654405.1 Mus musculus (house mouse) GI:16488233

COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
Tel: 81-45-503-9222
Fax: 81-45-503-9216 230-0045, Japan

Email: genome\_res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., System--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res.

sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

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RESULT 32
CD551263
LOCUS
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AUTHORS
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                           Bource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                                                                                                                                                                                       Laboratory of Genetics
National Institute of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0325 row: H column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD551263
CD551263.1 GI:31598994
EST.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 604)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD551263 604 bp mRNA linear B0325H01-5 NIA Mouse E9.5 Whole Embryo cDNA Library musculus cDNA clone NIA:B0325H01 IMAGE:30431508 5',
                                                                                                                                                                                         Seq primer: M13 Reverse
High quality sequence s
                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 11 (9),
21429098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   further details.
                                                                                                                                                                                                                                                                                                                                        Contact: Dawood B. Dudekula
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                11544199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCTACCACATCCACTGCCTGAACCCCCCCCCCGCTGCCAGAGATCCCAAACGGCGAATGGCT
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                                                                                                                                                                                    quality sequence stop: 604
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/clone_lib="RIKEN full-length enriched, 2 days neonate
thymus_thymic_cells"
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                 /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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                                                                                                                                          Location/Qualifiers
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clone="NIA:B0325H01 IMAGE:30431508"
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Pred. No. 0.0016;
0; Mismatches 43;
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RESULT 33
CK781630
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin Unive
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CK781630 625 bp mRNA UI-M-HEO-clz-o-ll-0-UI.rl NIH_BMAP_HEO Mus IMAGE:30630778 5', mRNA sequence.
                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 625)
                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and purified by ethanol precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total Genome Res. 11: 153-1558 (2001) [PMID: 11544199]). Total RNAs were extracted from a pool of 16 embryos at 9.5-days
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/dev_stage="whole embryo includir
at 9.5-days postcoitum"
/lab_host="DH10B"
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Pred. No. 0.0016;
0; Mismatches 43;
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clone was contributed by the Brain Molecular Anatomy Project

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REFERENCE
AUTHORS
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BU705998
LOCUS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 bp
UI-M-FOO-caa-i-lO-O-UI.T1 NIH BN
IMAGE:6408657 5', mRNA sequence-
BU705998
                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 634)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BU705998.1 GI:23636034
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Seq primer:
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/dev stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="Ph108 (T1 phage resistant)"
/clone_lib="NIH_BMAP_HEO"
/clone_lib="NIH_BMAP_HEO"
/note="Organ: Eye; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lemmon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyX-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
clone was contributed by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6"
/db_xref="taxon:10090"
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BMAP_FOO Mus musculus cDNA clone
Brain Molecular Anatomy Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 TTCCTACCACATCCACTGCCTGAACCCCCGCTGCCAGAGATCCCAAAACGGCGAATGGCT
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagg.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UI-M-FO0-bzp-b-16-0-UI.rl NIH_BMAP_FO0 Mus musculus IMAGE:6405423 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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//lab host="DH10B (T1 phage resistant)"
//clome lib="NIH_BMAP FOO"
//clome lib="NIH_BMAP FOO"
//clome lib-min Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I and Soares, Genome Research, 6: 791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
grimer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGACAGAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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/mol type="mRNA"
/strain="C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:6408657"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Socation/Qualifiers
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Pred. No. 0.0016;
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RESULT 36
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TITLE
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , 68
                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                  Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 723)
                                                                                                                                                                                                                                                                                                                                                                                                          CB246896.1 GI:28368540 EST.
Mus musculus (house mouse)
                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB246896
UI-M-FIO-cdy-k-21-0-UI.r1 NIH
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                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE: 6836206 5',
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  clone was
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primer containing a Not I site. Double strand CDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library teg
sequence located between the Not I site and the polyA tail
is TGAGACAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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/lab_host="DH10B (Tl phage resistant)"
/clone_lib="NIH_BMAP_FOO"
/clone_Tib="NIH_BMAP_FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
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67.4%;
contributed by the Brain Molecular Anatomy Project
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Pred. No. 0.0016;
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REFERENCE
AUTHORS
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CF726532
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Best Local Similarity
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                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 730)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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UI-M-HB0-ckh-h-09-0-UI.r1 NIH_BMA
IMAGE:30547664 5', mRNA sequence.
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Seq primer: pYX-5.
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                                                                        This clone was contributed by the Brain Molecular Anatomy Project
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//dev_stage="mbhyo 12.5dpc"
//lab_host="DH10B (T1 phage resistant)"
//clone lib="NIH BMAP FI0"
//clon
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/tissue_type="whole_brain"
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ACCESSION
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CN534827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CN534827
CN534827.1 GI:46862983
EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN534827 736 bp mRNA linear EST 29-APR-2004 UI-M-HS0-cqd-k-04-0-UI.rl NIH_BMAP_HS0 Mus musculus cDNA clone IMAGE: 10674835 '5', mRNA sequence.
                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
Clone Distribution: Distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 736)
Seq primer: pYX-5.
Location/Qualifiers
1. .736
                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                           This clone was contributed by the Brain Molecular Anatomy Project
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/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab host="DH10B (T1 phage resistant)"
/lab host="DH10B (T1 phage resistant)"
/cloine=lib="NIH_BMAP_HB0"
/cloine="Organ: Eye; Vector: pyx- Asc; Site 1: BcoR I;
/note="Organ: Eye; Vector: pyx- Asc; Site 1: BcoR I;
/site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mENA size fraction, ligated
with EcoR I adaptor , digested with Not1 and then cloned
directionally into pyx-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.ulowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 754)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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EST.
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                                                                                                                                                         Seq primer: pYX-5.
Location/Qualifiers
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/clone lib="NIH BMAP HS0"
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/note="Organ: Upper Head; Vector: Upper Head; Vector
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/db_xref="taxon:10090"
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/mol_type="mRNA"
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TITLE
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CN536888
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EST.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                  Seq primer: pYX-5
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                                                                                                                                                                                                                       clone was contributed by the Brain Molecular Anatomy Project
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="+~~
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/dev gtage="9.5-10.5 dpc"
/lab_host="915-10.5 dpc"
/lab_host="DH1OB (T1 phage resistant)"
/clone_lib="NHH_BMAP_HOO"
/note="0rgan: Head; Vector: pX-Asc; Site_1: EcoR I;
/note="0rgan: Head; Vector: pX-Asc; Site_1: BcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
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/db_xref="taxon:10090"
/clone="IMAGE:30638082"
                                                                                    organism="Mus musculus"
                                                                                                                                      Socation/Qualifiers
           xref="taxon:10090"
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Pred. No. 0.0017;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                             source
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
B 1 (bases 1 to 762)
NII-McC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC Clone distribution information can be
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UI-M-FYO-ccw-f-03-0-UI.rl NIH BMAP_FYO
IIMAGE:6825316 5', mRNA sequence.
CA327845
CA327845 GI:24545943
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                                                                                                                                                                             Seg primer:
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/organism="Mus musculus"
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/strain="C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:6825316"
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/lab_host="DH10B (TI phage resistant)"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP HO0"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
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Pred. No. 0.00:
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                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consorthum/LLNL at:
http://image.llnl.gov
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CA749488.1 GI:25571583
EST.
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UI-M-FYO-cdd-n-01-0-UI.rl NIH_BMAP_FYO Mus
IMAGE:6831650 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 768)
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Mational Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                        Seq primer: pYX-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab host="DH10B (TI phage resistant)"
/clome_lib="NIH_BMAP_FYO"
/clome_lib="NIH_BMAP_FYO"
/clome_lib="NIH_BMAP_FYO"
/clome_lib="NIH_BMAP_FYO"
/note="COrgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="COrgan: Brain; Vector: pYX- Asc primed with Oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX- Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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                                                                                                                                                                                                                             clone was contributed by the Brain Molecular Anatomy Project
                                          /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6831650"
                                                                                                organism="Mus musculus"
                                                                                                                                                  Location/Qualifiers
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0; Mismatches 4
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RESULT 42 CA749488

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                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 787)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CK637900 787 bp mRNA
UI-M-HOO-cnt-m-12-0-UI.r1 NIH_BMAP_HOO
IMAGE:30642251 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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Similarity 67.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGAGCTCCTGTGCTGTGACACATGCCCTTC
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/clone_lib="NIH_BMAP_RYO"
/clone_lib="NIH_BMAP_RYO"
/note="Organ: Brain; Vector: pyX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                         clone was
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30642251"
                                                                                                                                                      uocation/Qualifiers
l. .787
                                                                                                                          organism="Mus musculus"
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                                                                                                                                                                                                                                                                         contributed by the Brain Molecular Anatomy Project
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Pred. No. 0.0017;
0; Mismatches 4
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musculus
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CDNA clone
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 799)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CA752497.1 GI:25583236
EST.
Mus musculus (house mouse)
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UI-M-FO0-cdo-p-13-0-UI.r1 NIH
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                                                                                                                                                                                                                                         Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE:6831326 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                  clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with BCOR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP); 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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/lab_host="NIH BMAP HOO"
/clone lib="NIH BMAP HOO"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarage
                                                /db_xref="taxon:10090"
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/strain="C57BL/6"
                                                                                                                                                                                                                  Location/Qualifiers
                            tissue_type="whole brain"
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No. 0.0017;
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REFERENCE AUTHORS TITLE

COMMENT

JOURNAL

FEATURES

/dev\_stage="embryo 12.5dpc"

ACCESSION VERSION

ORGANISM

DEFINITION

RESULT 44 CA752497

ફ 밁 Ś 밁 ঠ ORIGIN

Matches

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REFERENCE
AUTHORS
TITLE
JOURNAL
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VERSION
KEYWORDS
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BQ771341
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                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 832)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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UI-M-FIO-byu-a-09-0-UI.rl NIH_BMAP_FIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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/clone lib="NIH BMAP FOO"
/note="Organ: Brain; "Vector: pXX- Asc; Site_1: EcoR I;
/note="Organ: Brain; "Vector: pXX- Asc; Site_1: The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGAGCC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                  clone was contributed by the Brain Molecular Anatomy Project
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/db_xref="taxon:10090"
/clone="IMAGE:5702288"
/tissue_type="whole brain"
                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                  Location/Qualifiers
                                                                             strain="C57BL/6"
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Pred. No. 0.0017;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENCOURT 8750481 NIH MGC 130 5', mRNA sequence.
BU152563
BU152563.1 GI:22666095
                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAN13791 row: m column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                      High quality sequence stop: 440.
                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACGAC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_130"
/note="Organ: otocysts; Vector: pCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="DH10B (T1 phage resistant)"
/clome_lb="NIH_BMAP_F10"
/note="Organ: Brain, Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6333110"
                                                                                                                                                                              organism="Mus
                                                                                                                                                                                                                                        ocation/Qualifiers
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Pred. No. 0.0017;
                                                                                                                                                                                 musculus"
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Vector: pCMV-SPORT6.1; Site_1:
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DEFINITION BU152563 RESULT 46

SOURCE

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RESULT 47
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Matches
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TITLE
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Best Local Similarity
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                       Local
                                                                                                                                                                                                                                                                                                        Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila NNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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     120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metzaoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNS006XK 935 bp DNA linear GSS 03-JUN-19 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL066051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                         Similarity
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                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                   /note="end : T7"
                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                         1. .935
                                                                                                                                                 clone_lib="RPCI-98"
                                                                                                                                                                      /db_xref="taxon:7227"
/clone="BACR14N09"
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Score 63.2; DB 9;
Pred. No. 0.0017;
7; Mismatches 189;
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Pred. No. 0.0017;
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survey sequence T7 end of BAC #
  189;
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Indels
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CR715927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CR715927 1066 bp Tetraodon nigroviridis full-length CR715927 GR715927.1 GI:51214161 HTC; cDNA; full-length; Tetraodon r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences are based on single pass reads. More information available at http://www.genoscope.cns.fr/tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCCCGCCCGCCTGGCCCTGGGCCTGCCAAGGATGACACTGCCAGTCACGAGCCCGC 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGTGTCCACCAATGAAGGGGAAAGTTCAGAAAGTTTTAACTTGGCGATGGGGGGACCCA
                                                                                                                                        GCCTGCCTGTCCCCTCCGGGGGGGGGTCCCAGTGGGACCTGGAGGTGCTCCAGCTGC
                                                                                                                                                                                   GTGTGCAAGGATGGAGGAGAGCTGTTGTGCTGTGACACCTGCCCCCTCCTACCACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGGGCCATCCAGAGCATGGCCCGTCCGGCGGCCCCCTTCCCCTCC 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGCACAGGGATGACCTGGAGTCCCTTCTGAGCGAGCACACCTTCGATGGCATCCTGCA 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGGCGSCGCSCSSCGCGSGCSSGSSGCSCCSCCSSSSGSCCSCGCGCGCGMSMCSG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGCTGCAGATCCTGCTCAGGAGACGTGACCCCAGCCCCTGTGGAGGGGGGTGCTGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCTGCCTTCCACTGGCGCTGCCACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTGCGCGTTGCGGGGTGTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYMSSSVSCCSCSGTCCGYCSSCTSCKMCSCTYGCKCGCGCGCSTSCSSSSCCSBBSYST
                                                         CTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCGGCCCCAGGAGCCA
                                                                                                                                                                                                                          GIGIGICGGGACGGGGGAGCTCATCTGCTGTGACGGCTGCCCTCGGGCCTTCCACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGGCGSCCSGGGCGCSSSCSGCGCGSGGSSCCGSGCGSGCGSGSSGGGSSSSGSGSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1066)
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Eggs"
                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:47144"
                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Tetraodon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                   4.1%;
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                                                                                                                                                                                                                                                                Score 63.2; DB 3; Pred. No. 0.0017; 0; Mismatches 88;
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cDNA
                                                                                                                                                                                                                                                                    88;
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                             Group Phase I & II Team
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3137)

8 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hayashida, K., Hayatsu, N., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A.,
Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RIKEN Genome Exploration Research Group Phase
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ency full-length cDNA
ol. 303, 19-44 (1999)
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mrna linear HTC 03-APR-2004
Mus musculus 12 days embryo embryonic body between diaphragm region
and neck cDNA, RIKEN full-length enriched library, clone:9430004K15
product:CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2
AUTOANTIGEN 218 KDA PROTEIN) (MI2-BETA) homolog [Homo sabiens]
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)

Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Nagaoka, S., Sasaki, N., Carninci, P., Kitsunai, T., Tashiro, H., Itoh, M., II Team

The FANTOM Consortium and the RIKEN Genome Exploration Research annotation of a full-length mouse cDNA collection

Carninci, P.

Submitted (16-JUL-2001) Yoshihide Hayashizaki,

Sakazume, N.,

Ohsato, N.,

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FEATURES
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Best Local Similarity
Matches 89; Conserv
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CDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                              GGCCTTCCACCTGGCCTGCCCTGCCCTCCGCTCCGGGAGATCCCCCAGTGGGACCTGGAG
                                                                GTGCTCCAGCTG
                                                                                                                              TTCCTACCACATCCACTGCCTGAACCCCCCCCCCGCTGCCAGAGATCCCCAAACGGCGAATGGCT
                                                                                                                                                                                                                                                            GGAATTCTGTCGCGTCTGCAAGGACGGCGGGGAGCTCCTGTGCTGTGACACATGCCCTTC 643
                                                                                                                                                                                                                                                                                                                   GGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
CIGICCCCGCIG
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PKPLEGRPERQPFVKNGMSYNHCSWYSELQLELHCQVNERNYQRKNUNDEPPSCDFG
GDEBKSRKRKNCNCDPKPAEMBERFYRYGIKPEMMOHTRILMSUDKKGHVHYLIKWRDL
PYDQASWESEDVEIQDYDLFKGSYWNHRELMRGEEGRPGKKLKKYKLRKLERPPSTFT
VDPTVKYERQPEYLDATGGTIHPYQMECLNWLAFSWAQCTDTILADEMGLGKTVQTAV
FLYSLYKEGHSKGPFLVSAPLSTIINWEREFEMMPDMYVVTYVGDKDSRAIIRENEF
SFEDNAIRGGKASRMKKEASVKFHVLLTSYELITIDMAILGSILPERPADI
AKEDQIKKLHDMLGPHMLRRLKADVFKNMPSKTELIVRVELSPMQKKYYKYILTRNFE
ALMARGGGNQVSLLNVVMDLKKCCNHPYLFEVAAMEAPKNPMGWTDGSALTRAGGKLL
LLOKMLKNLKEGGHRVLIFSOMTKMLDLEDFLEHEGYKVERIDGGITGNMRQBATDR
FNAPGAQQPCFLLSTRAGGLGINLATADTVIIYDSMAPHNDIQAFSRAHRIGQNKKV
MIYRFVTRASVEERITQVAKKKMMLTHLVVRPGLGSKTGSMSKGELDDILKFGTEELF
KDBATDGGGDNKEGEDSSVIHYDDKAIERLLDRNQDETEDTELGGMNEYLSSFKVAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unnamed protein product; CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN 218 KDA PROTEIN) (MI2-BETA) homolog [Homo sapiens] (SWISSPROT [Q14839, evidence: FASTY, 99.8%ID, 54.6%length, match=3135)
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EVTAVDGYETDHQDYCEVCQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCE
KEGIQWEAKEDNSEGEEILEEVGGDPEEEDDHHMEFCRVCKDGGELLCCDTCPSSYHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=3
/protein_id="BAC28749.1"
/db_xref="GI:26330021"
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/dev_stage="12 days embryo"
<1. .->3137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="PIRKAKTKEGKGPNARRKPKGSPRVPDAKKPKPKKVAPLKIKLG"
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|mol_type="mRNA"
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_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%;
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                                                             664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                          43;
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Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               916
616 SVSASSGMSSSVSSSGGRSSGSGGGGGGGGGSGSGSGSGGSGGSGSVCSCSSGCMCRCSC
                                                                                                                                                                               796
                                                                                                                                                                                                                                                                                                                      856 KCNASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGSGGASASHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436 GCTGGGGGAGCTGTTTTGGGAAGGAGGTGGCTCTCAGGAGGGTGCTGCACCCCAGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly), genomic AL053013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS0091P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly
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                                        CCCCGCTCCCCCGGGGCTTAGGTCGGCGGGAGAGGAGGTAAGAGGTCCACCTGGGGAAC
                                                                                      CAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCCGGGCCCCAGGAGCCACCCGTGGAGA
                                                                                                                                                                                                                                                                        TCTGCATGGGCGTCTCTTGCCTGTGCCAGAAGAATGAGGACGAGTGTGCCGTGTGTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_rref="taxon:7227"
/clone="BACR19D16"
/clone_ib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:4934461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%; Score 62.8; DB 9; Length 925;
13.3%; Pred. No. 0.0021;
tive 181; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
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survey sequence TET3 end of BAC #
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RESULT 51
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JOURNAL
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Best Local
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                                                   543
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                                                                                                                                                                                                                                                                                   528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       796 CCCTAGCCGGCATGGACACGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute). DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Sandy Clifton, Ph.D.
WashU Xenopus BST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bor Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McWaterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
Unpublished (1999)
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GAG29408.yl Wellcome CRC pCS107 tropicalis St10-12 Xenopus tropicalis cDNA clone IMAGE:4440999 5' similar to TR:095884 095854

TRANSCRIPTIONAL INTERMEDIARY FACTOR 1 ALPHA. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Library constructed by A. Zorn and J. Mason (Wellcome/CRC
Institute). DNA Sequencing by: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 587)
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EST.
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                                                TGGATCTGCACCTTTTGCCGGGACCTGTCCAGACCAGAAGTGGAG
                                                                                            TGGAGGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAG
                                                                                                                                                                                    CTTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGCTCCGGGAGATCCCCCAGTGGGACC 647
                                                                                                                                                                                                                                     AATGAGGACTGGTGTGCTGTATGTCATAATGGGGGGGAGCTGCTTTGCTGAAAAAATGT
                                                                                                                                                                                                                                                                                 AATGAGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGC 587
                                                                                                                                           CCCAAAGTTTTCCACCTGTCGTGCCACGTGCCTACACTGATGAACTTTCCCAGTGGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 502.
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4440999"
/tissue_type="whole embryo, stages 10-12"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC pCS107 tropicalis St10-12"
/note="Vector: pCS107; Site 1: NotI; Site 2: EcoRI; CDNAs were oligo-dT primed and directionally cloned. Average insert size 1.5 kb, range 0.5-4 kb. Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
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                                                                                                                                                                                                                                                                                                                                                     4.1%;
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                                                                                                                                                                                                                                                                                                                               Pred. No. 0.00
); Mismatches
                                                                                                                                                                                                                                                                                                                                                       Score 62.6; DB 4
Pred. No. 0.0022;
                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                             Length 587;
                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 53
CB523529
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REFERENCE
AUTHORS
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VERSION
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SOURCE
ORGANISM
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CN526117
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Best Local S
Matches 88
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                                                                                                                                              593 GGCCTTCCACCTGGCCTGTCCCCTCCGGCTCCGGGAGATCCCCAGTGGGACCTGGAG
                                                                                                                                                                                                             506
626 CTGTCCCCGCTG 637
                                                                                                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Diatribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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CN526117
CN526117.1 GI:46853770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN526117 677 bp mRNA linear BST 29-APR-
UI-M-HNO-coc-j-05-0-UI.rl NIH BMAP HNO Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                           GGACGAGTGTGTGTGTGGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTCG 592
                                                   GTGCTCCAGCTG
                                                                                                     TTCCTACCACATCCACTGCCTGAACCCCCCCCCCCGCTGCCAGAGATCCCANACGGCGAATGGCT
                                                                                                                                                                                                          GGAATTCTGTCGCGTCTGCAAGGACGGCGGGAAGCTCCTGTGCTGTGACACATGCCCTTC 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 677)
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Upper Head"
/dev stage="9.5-10.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP HN0"
/clone lib="NIH BMAP HN0"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand CDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand CDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                        4.0%;
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                                                                                                                                                                                                                                                                                                                  Score 62.2; DB 7
Pred. No. 0.0028;
0; Mismatches 4
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COMMENT

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UI-M-GH0-cer-1-07-0-UI.r1 NIH BMAF
IMAGE:6843512 5', mRNA sequence.
CB523529
CB523529.1 GI:29356884
EST
Mus musculus (house mouse)
Mus musculus
                                                                                                                                           602
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Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
  BU056500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone was contributed by the Brain Molecular Anatomy Project
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                                                                                                                                           CTGTCCCCGCTG 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:6843512"
/tissue_type="Whole brain"
/teyset=ge="1, 5, and 15 days newborn"
/dev_stage="1, 5, and 15 days newborn"
/lab host="MIHB (TI phage resistant)"
/clone_lib="NIH_BMAP_GHO"
/clone_lib="NIH_BMAP_GHO"
/clone_rorgan: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according
BonaTdo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Io

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UI-M-FOO-cab-h-16-0-UI.rl NIH_BMAP_FOO Mus musculus cDNA clone IMAGE:6409023 5', mRNA sequence.
BU056500
BU056500.1 GI:22496577
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
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//dev stage="embryo 12 Sago"
//lab host="0H108 (T1 phage resistant)"
//clone_lib="NIH_BMAP_FOO"
//clone_lib="NIH_BMAP_FOO"
//clone_lib="NIH_BMAP_FOO"
Site_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed on a 1% agarose
genaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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Pred. No. 0.0028;
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R.Site 1
R.Site 2
 tigr-gss-dog-17000326704476 Dog Library Canis familiaris genomic, genomic survey sequence.
CE173623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tibrary availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    natiori,M., Toyoda,A., Noguchi,H.,
BAC end Sequences of Library MSMg01
Unpublished
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AG561783
AG561783.1 GI:48322481
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                                                       CE173623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 776)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e-mail: abe@rtc.riken.jp
                                                                                                                                                                                    TGAGGGTCAGC 921
                                                                                                                                                                                                                                                           GGAGCCCAAAGCCAGCTCTGATGCTGCTGTCACATATGTGAACCTGCTGGCCCCCACACCC
                                                                                                                                                                                                                                                                                                                                                                      GGAATTCCAGATCCTCGTGGGACTGAGGTCAGCTTCAGAGAAAACCAGGGGCCCCGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus molossinus"
/mal_type="genomic DNA"
/sub_specises="molossinus"
/db_xref="taxon:57486"____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="MSMg01-481F17.TJ"
|sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : pBACe3.6
: EcoRI
: EcoRI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 61.8; Di
; Pred. No. 0.00;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 776;
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                                                       GSS 25-SEP-2003
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BE234617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kirkness EP
The Institute for Genomic
Department of Eukaryotic G
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 434) Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, Quackenbush, J. and Keele, J.W. Porcine gene discovery by normalized cDNA-library se EST cluster assembly Mamm. Genome 13 (8), 475-478 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 262)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                BE234617 434
141780 MARC 1PIG Sus scrofa o
BE234617
Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                             Sus scrofa
                                                                                                                                                                                                                                                                            Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                              BE234617.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CE173623.1 GI:35316113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14512627
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                                                       12226715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCTCCAGCTG 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCTACCACCTGCACTGCCTCAACCCGCCGCCGCGAGATCCCAAACGGTGAATGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGTTCTGCCGCGTGTGCAAGGACGGCGGCGAGCTGCTCTGCTGCGACGCGTGCCCCTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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Pred. No. 0.0034;
0; Mismatches 4
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sequence.
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                                                                                                                                                                                                                         Euteleostomi;
Sus.
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CF792818/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 AATGAGGACGAGTGTGCCGTGTGTCCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                CF792818 670
885797 MARC 4PIG Sus scrofa c
CF792818 CF792818.1 GI:37797379
EST.
cross_match v0.990329.
Plate: TMW8013 row: I column: 11
Seq primer: TAGAAGGCACAGTCGAGG.
                                                       Single pass sequencing. Bases called with trimmed with the aid of the trim_alt optic
                                                                                         Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                       Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                  I (bases 1 to 670)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed
embryos representing early developmental stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 79 row: P column: 20
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and -minmate
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.989904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (pig)
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Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
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/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="MARC IPIG"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2:
Library made from pooled tissue from day 11, 13, 1
and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
/mol_type="mRNA"
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57.6%;
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Pred. No. 0.004;
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                                                           with phred v0.020425.c and option. Vector identified v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81,
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                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Sus.
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RESULT 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Nonneman,D.J., Wray,J.E. and Keele,J.W.
Porcine EST collection using a normalized library combryos representing early developmental stages Unpublished (2003)
                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified v cross match v0.990329.
Plate: TMW8013 row: I column: 11
Seq primer: GTAATACGACTCACTATAGGG.
LOCALION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             889669 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                              Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Smith
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/clone_lib="MARC 4FIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="MARC 4PIG"
/note="Vector: pcDNA3.; Site_1: EcoRI; Site_2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                            /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
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/mol_type="mRNA"
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Pred. No. 0.0042;
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Sus.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Nonneman, D.J., Wray, J.E. and Keele, J.W.

Porcine EST collection using a normalized library ocembryos representing early developmental stages Unpublished (2003)
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Plate: TMW8048 row: N
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                         AATGAGGACTGGTGTGTGTGTCAGAACGGGAACTCCTGTGCTGTGAGAAGTGT
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   CCTCGGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACC 647
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                                                                                                                                                                                                                                                                                                                  /clone lib="MARC 4PIG."
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site
Library made with combined RNA from day-10, d
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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Pred. No. 0.0042;
                                                                                                                                                                                                   Score 61.4; DB 7
Pred. No. 0.0043;
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Sus.
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Unpublished (1999)
Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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BG307509 mRNA linear EST 22-FEB-;
f159a10.x1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone
IMAGB:3818011 3' similar to SW:CHD4 HUMAN Q14839 CHROMODOMAIN
HELICASE-DNA-BINDING PROTEIN 4 ;, mRNA sequence.
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1 (bases 1 to 520)
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Danio rerio
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Seq primer: T7 from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.
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                                                                           /dev stage="adult"
//dev stage="adult"
//dev stage="BH10B (phage resistant)"
//clone lib="Sugano Kawakami zebrafish DRA"
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unfertilized eggs)"
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/strain="AB"
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      DB 4;
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RESULT 62
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                          -22 Suehiro-cho, '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 ATCCACTGCACTGCACCCCCCCGCTGCCAGAGATCCCCAAAGGGCGAATGGCTCTGTCCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 CTGGCCTGCCTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 GCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGACGGCTGCCCTCGGGCCTTCCAC 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 804)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    804 bp mRNA linear EST 29-APR. UI-M-HS0-cqi-o-05-0-UI.rl NIH BMAP_HS0 Mus musculus cDNA clone IMAGE:30674548 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CN535140
CN535140.1 GI:46863296
                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details.
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                            primer: pYX-5.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                          clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="blastocyst"
/clone_lib="RIKEN full-length enriched, blastocyst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60.8; DB Pred. No. 0.0055
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gooegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            545
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AL066051.1 GI:4945019
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
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/clone lib="NIH BMAP HS0"
/clone lib="NIH BMAP HS0"
/note="Organ: Upper Head; Vector: pYX-Asc; Site_1: EcoR I;
/note="Organ: Upper Head; Vector: pYX-Asc; Site_1: EcoR I;
/note="Corgan: Upper Head; Vector: py
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
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/dev_stage="embryo 9.5 - 10.5 dpc"
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Pred. No. 0.
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segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 64 CNS006XK/c

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                                                                                                                      JOURNAL
MEDLINE
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Best Local Similarity
                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                      PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 GGCTTAGGTCGGCGGGAGAGGAGGTAAGAGGTCCACCTGGGGAACCCCCTAGCCGGCATGG
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1. (bases 1 to 359)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         BE814801
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QV4-BN0090-020600-236-g06 BN0090
                Brazil
                               Rua Prof. Antonio
                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                    Contact: Simpson A.J.G.
                                                                                                                                       Proc. Natl.
                                                                                                                                                       sequence tags
                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                          Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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Tel: +55-11-2704922
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/db_xref="taxon:7227"
/clone="back14N09"
/clone lib="RPCI-98"
/note="end: T7"
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Pred. No. 0.0074;
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ORGANISM
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CF137810
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Best Local 9
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cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
                                                                                                               Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Louis Staudt
                                                                                                                                                                                                        Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 bp
UI-HF-BNO-ank-f-11-0-UI.r1 NIH N
IMAGE:3093236 5', mRNA sequence
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-BN0090-020
600-238-906&t3=2000-06-02&t4=1)
Seq primer: puc l8 forward
High quality sequence stop: 359.
                                                                                                                                                                                                                                                                                                                                                                          discovery
                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 461)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                   Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone lib="RN090"
/clone lib="RN090"
/note="Organ: breast normal; Vector: puc18; Site_1: SmaI;
/site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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/mol_type="mRNA"
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                                                                                           University of Iowa
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                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov

Bco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consorthum/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 544)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU429642
UI-HF-BNO-aek-f-09-0-UI.r2 NIH_MGC_50 Homo sapiens
IMAGE:3064481 5', mRNA sequence.
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                                                                                                                                                                                                                                 Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%;
ilarity 61.5%;
Conservative
/tissue_type="lymph"
/cell_type="germinal center
/cell_line="MGCBS"
/lab_host="DH10B (LTI)"
/clone_lib="NHH_MGC_50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab Nost="DHIOB (LTI)"
/clone_lib="NIH_MGC_50"
/clone_lib="NIH_MGC_50"
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
Constructed from sic fractionated cytoplasmIc mRNA
Constructed from sic fractionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:3064481"
                                                                                                                                                                                                            Location/Qualifiers
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/cell_type="germinal center B cells"
/cell_line="MGC85"
/cell_line="MGC85"
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/db_xref="taxon:9606"
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Pred. No.
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National Eye Institute
6/331, NIH, Bethesda, MD 20892-
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593 bp
hw37c03.y1 Human primary human
Homo sapiens cDNA clone hw37c03
CN483764
CN483764.1 GI:46565268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: graeme@helix.nih.gov
Plate: 37 row: c column: 03
Seq primer: M13RP1 reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 593)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tag analysis of cultured primary human ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsai, J.Y. and Wistow, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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/note="Organ: Eye; Vector: pSport1; RNA was extracted from primary human pericytes in culture. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGATCGCGAGCGGAGCGGCCCCT]15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed at the NIH Intramural Sequencing Center (NISC)."
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                                                                                                                                                                                                                                                                          /clo\overline{n}e lib="Human primary human ocular pericytes. Unampl\overline{l}fied (hw)"
                                                                                                                                                                                                                                                                                                                    /cell_type="pericytes"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hw37c03"
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hw37c03 5', mRNA sequence.
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143
                                                                                   532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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                                                                                                                              96;
                                                                                                                                                                                                                                                                                                                                                                                                               Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
Virology, Institute of Medical Science, University of Toky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helix Research Institute
1532-3 Yana, Kisarazu, Cl
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRI human cDNA project Unpublished (2000)
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1 (bases 1 to 683)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-438-52-3986
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GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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                                                                                                                                Conservative
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                                                                                                                                                                                                             /cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_line="NT2RP2"
/clone_tine="NT2RP2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal
cells after 2-weeks retinoic acid (RA) induction
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2001829"
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                                                                                                                            Score 60; DB Pred. No. 0.000
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Pred. No.
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0.0087;
                                                                                                                                               0.0088
                                                                                                                                                                DB 1;
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                                                                                                                                                             Length 683
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BG329665
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KEYWORDS
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Best Local Similarity
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                                                                                                                                                                                               652 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
                                                                                                                                                                                                                                                                           592
                                                                                                                                                                                                                                                                                                                                                   532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                              96;
      BE258675 700 bp mRNA linear EST 13-JUL-2: 6011116344F1 NIH MGC_16 Homo sapiens cDNA clone IMAGE:3358962 5', mRNA sequence.
BE258675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov Plate: LLCM1265 row: h column: 20 High quality sequence stop: 650.
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1 (Dases 1 to 699)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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EST.
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                               GGGCCTTCCACCTGGCCTGCCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                                                                               AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                          GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG
                                                                                                                                                                                                                                     GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/clone libb="NH10B (phage-resistant)"
/clone libb="NH1MGC 16"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE: 4558915"
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Pred. No. 0.0088;
0; Mismatches 60; Indels
                                                            EST 13-JUL-2000
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Best Local S
                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 731)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Galdman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                     BE176589
RC3-HT0585-010400-023-c04
BE176589
                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                             Homo sapiens (human)
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EST.
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                                                                                                                                                                                                                                                                   731 bp mRNA linear
HT0585 Homo sapiens cDNA,
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mRNA sequence. EST 21-JUN-2000

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190 GCTGCCCACACTGCGAGAAGGAAGGCATCCAGTGGG
                                                                652 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG 687
                                                                                                                                                     130 GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                             592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM163 row: g column: 11.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1 (bases 1 to 700)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                              AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_hoBt="DH10B (phage-resistant)"
/clone lib="NH10B (phage-resistant)"
/clone lib="NIH_MGC 16"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
/coned into EcoRI/XhoI sites using the following 5;
/cloned into EcoRI/XhoI sites using the following 6;
/cloned into EcoRI/XhoI sites using the following 4;
/cloned into EcoRI/XhoI sites using Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3356962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="retinoblastoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 2; Length 700; Pred. No. 0.0088;
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225
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AUTHORS
TITLE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                    BE297517 750 bp mRNA linear BST 20-JUL-2: 601178063F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533391 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=RC3-HT0585-010400-023-c04kt3=2000-04-01&t4=1)
                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 750)
                                                                                                                                                                                                                                                                    BE297517
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                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                BE297517.1 GI:9181002
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="HT0585"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
/note="Rogan: head neck; Vector: puc18; Site_1: SmaI;
/note="Rogan: head neck; Vector: puc18; Site_1: SmaI;
/note="Rogan: head neck; Vector: was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="HT0585"
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Preparation: Ling Hong/Rubin Laboratory
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                                                                                             Collection
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AUTHORS
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BE259148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE259148 817 bp mRNA linear EST 13-JUL-20
GRILL 18075F1 NIH MGC_16 Homo sapiens CDNA Clone IMAGE:3344251 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: LLCM210 row: n column: High quality sequence stop: 550.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                                      CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCM130 row: e column: 20.
Location/Qualifiers
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/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_17"
/clone_lib="NIH MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally_cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 0.0089;
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REFERENCE
AUTHORS
TITLE
JOURNAL
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KEYWORDS
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Best Local Similarity
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13503 row: e column: 14
High quality sequence stop: 649.
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AGENCOURT 7892893 NIH_MGC_72
5', mRNA Bequence.
B0437443
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BQ437443.1 GI:21176519
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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/lab host="PH10B (phage=resistant)"
/clone_lib="NH10B (phage=resistant)"
/clone_lib="NH MGC Li6"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                              /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
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/tissue_type="melanotic melanoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
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  3.9%;
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  Score
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  60;
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5
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Length 878;
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Best Local Similarity
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                                                                                                                  532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGAGCTCATCTGCTGTGACGGCTGCCCTC 591
                                         592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCCAGTGGGACCTGGA 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
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64
                                                                                                                                                                              96;
                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 948)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM54 row: c column: 23 High quality sequence stop: 746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600944490F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960590 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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GTGCTTACCACATGGTCTGCCTGGATCCCGACATGGAGAAGGCTCCCGAGGGCAAGTGGA
                                                                                      AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
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                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                              /clone="IMAGE:2960590"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 17"
/clone_lib="NIH MGC 17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally_cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 0.0091;
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  989 bp
AGENCOURT_6406806 NIH_MGC_92 Homo
5', mENA sequence.
BM457082
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1 (bases 1 to 974)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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BG394104.1 GI:13287552
EST.
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602456272F1 NIH_MGC_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                            AGGACTATTGCGAGGTGTGCCAGCAAGGCGGTGAGATCATCCTGTGTGATACCTGTCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_16"
/clone lib="NIH_MGC_16"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:9606"
/clone="IMAGE:4579048"
/tissue_type="retinoblastoma"
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[mol_type="mRNA"]
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Pred. No. 0.0091;
0; Mismatches 60; Indels
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                                       mRNA linear E
sapiens cDNA clone
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                                         EST 05-FEB-2002
MAGE:5583326
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                                                         Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1011)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM12346 row: d column: 15
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                        BF309509.1
                                                                                                                                                                                                                                                                                                                      601892016F1 NIH_MGC_17 Homo
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Location/Qualifiers
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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llarity 61.5%;
Conservative
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/lab host="PH108 (phage-resistant)"
/clone lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; Oilgo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5583326"
                                                                                                                                                                                                                                                           GI:11256902
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Pred. No.
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Gaps

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Euteleostomi;

Homo

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REFERENCE
AUTHORS
TITLE
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BQ213031
LOCUS
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Best Local Similarity
Matches 96; Conserv
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AGENCOURT_7591269 NIH_MGC_92 Homo
5', mRNA sequence.
BQ213031
BQ213031.1 GI:20393828
EST.
               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLMM13346 row: h column: 04 High quality sequence stop: 446.
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1 (bases 1 to 1365)
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                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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/tissue_type="rhabdomyosarcoma"
/tissue_type="rhabdomyosarcoma"
/lab_host="ph108 (phage-resistant)"
/clone_lib="NIH_MGC_17"
/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by Controlof priming.
Site_1: XhoI; cDNA made bordord priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 0.0092;
0; Mismatches 6
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                                                                                                              This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-EN0063-301000-001-e05&t3=2000-10-30&t4=1)
Seq primer: puc ls forward
High quality sequence start: 14
High quality sequence stop: 426.
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                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laborzatory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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BF847408
                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
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/db xref="taxon.9606"

/clone="IMAGE:6067251"

/tissue type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone lib="NIH MGC 92"

/clone lib="NIH MGC 92"

/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: Sall; Cloned unidirectionally; oligo-dT primed.

Average insert size 2.5 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                           Location/Qualifiers
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Pred. No. 0.0095;
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EN0063 Homo sapiens cDNA,
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TITLE
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Best Local Similarity
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  Best Local Sim
Matches 103;
                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov blate: LLAM13474 row: k column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          885
AGENCOURT 7840454 NIH MGC_67
5', mRNA sequence.
BII 02516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 885)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                      Similarity
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    Conservative
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                                                                                               /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Adult"
/clone_lib="EN0063"
                                                                                                                                                                           /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
                                                                                                                                                                                                                                                                               organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                          clone="IMAGE:6146430"
                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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Score 59.8; DB Pred. No. 0.01; 0; Mismatches
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Pred. No. 0.0093;
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BU527069
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1 (bases 1 to 9.18)
NIH-MGC http://mgc.nci.nih.9ov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT 10155962 NIH MGC_101 Homo
IMAGE:6536820 5', mRNA sequence.
BU527069
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                Similarity
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GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
                                                                   GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
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                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_101"
/clome_lib="N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                            Score 59.8; DB Pred. No. 0.01;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 918;
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BU528543
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VERSION
KEYWORDS
                                                                    RESULT 85
BQ722521/c
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Best Local Similarity
Matches 103; Conserv
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BQ722521 1104 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8219490 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6188186 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM2703 row: c column: 08
High quality sequence start: 24
High quality sequence stop: 683.
Location/Qualifiers
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1 (Dases 1 to 943)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 10182979 NIH MGC 101 Homo
IMAGE: 6538496 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU528543.1 GI:22838984
EST.
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                                                                                                                                                                                                                                                                                       GGGCCTTCCACCTGGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                              GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCCGGGCAGAGGA 706
                                                                                                                                                                                                                                                            GTGCCTACCACCTCGTCTGCCTTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAATGGA
                                                                                                                                                                                                                                                                                                                                                       AGGATTACTGTGAGGTGTGCCAGCAGGGTGGGGAAATTATTCTGTGTGACACCTGCCCTC
                                                                                                                                                                    GCTGCCCTCACTGTGAGAAGGAGGGGGGGGCCCAAGGAGGAAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type-repidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 101"
/clone lib="NIH MGC 101"
/note="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
/note="CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="IMAGE:6538496"
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Pred. No. 0.01
0; Mismatches
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Best Local Similarity
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                                                                    1012 GCTGCCACTTCCCAGCCGGCACCTCCCGGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCT 1071
                                                                                                                                                                                                              892 CCCTACTGTGTGGGGTCCTGAGGGTCAGCAGAACCTGGCTCCTGGTGCGCGTTGCGGGG
                                                                                                                                                                                                                                                                                                           832 ACCTGCCGGCTCCGCCTTCTGCAGCCCCGCTGCCAGGTCTGGACTCCTCGGCCCTGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  772 AGGTAAGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712 GGCCCCAGGAGCCACCCGTGGAGACCCCGCTCCCCCGGGGCTTAGGTCGGCGGGAGAGG 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1104)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BQ722521.1 GI:21861418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ното варіепв
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                                                                                                                                                            TeTeCeGAGATEGTACEGACETECTECEGTETACTCACTECECCECTECCTTCCACTEGC
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                          quality sequence stop: 297.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Lupski_sympathetic trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Sit
Not1; Site 2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.8%; Score 59.4; DB 5;
41.8%; Pred. No. 0.013;
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BQ672163
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AGENCOURT_8302070 NIH_MGC_102 Homo
5', mRNA sequence.
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Plate: LLCM2457 row: g column:
High quality sequence stop: 306.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1132)
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BQ672163.1 GI:21782997
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National Institutes of Health, Mammalian
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                                                                                                 Similarity
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ATGAGAGAGTGCTGAGAAGGACACCTCCTTCCTCAGTCCTGGAAGC 1357
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                                                                         Conservative
                                                                                                                                                                             /clone="IMAGE:0274993"
/tlssue_type="epidermoid carcinoma, cell line"
/tlssue_type="epidermoid carcinoma, cell line"
/lab_host="BI10B (phage-resistant)"
/clone_lib="NIH_MGC 102"
/clone_lib="NIH_MGC 102"
/note="Organ: sallvary gland, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /moi_type="mRNA"
/db_xref="taxon:9606"
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Mismatches 592;
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5', mRNA Bequence.
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  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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Contact: Robert Strausberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                     AGAGGTCCACCTGGGGAACCCCTAGCCGGCATGGACACGACTCTTGTCTACAAGCACCTG
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                                     CACTTCCCAGCCGGCACCTCCCGGCCCGGGACGGGCCTGCGCTGCAGATCCTGCTCAGGA
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo caverage insert size 2 kb. Library constructed by Lift Technologies."
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/mol_type="mRNA"
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Pred. No. 0.02;
0; Mismatches 378;
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REFERENCE
AUTHORS
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CNS0072Q/c
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       Genoscope.
Direct Sub
                                               Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Budopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                 CNS0072Q 932 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                        fly), genomic survey sequence. AL066742 GI:4945205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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                                   (bases 1 to 932)
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: 805 447-4881
te: 00055 row: c cc
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Pred. No. 0.01
0; Mismatches
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1349
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532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB606244 416 bp mRNA line AMGNNUC:SRPB2-00055-Cl1-A srpb2 (10220) Rattus clone srpb2-00055-cl1 5', mRNA sequence.
                                                                                          GAGCCTACCATATGGTGTGCCTGGACCCCAGACATGGAGAAGGCCCCCCGAGGGCAAGTGGA
GCTGCCCACACTGTGAGAAGGAGGGTATCCAGTGGG
                               GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGG
                                                                                                                                      GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                    AGGACTATTGCGAGGTGTGCCAGCAAGGCGGCGAGATCATCCTGTGTGATACCTGTCCCC
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol type="mRNNA"
/mol type="mRNNA"
/db_xref="rtaxon:10116"
/clone="srpb2-00055-c11"
/tissue_type="prostate_tissue"
/clone_Tib="srpb2 (10220)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; rat prostate normalized double selected poly(A+) mRNA size fraction > 1 kb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thousand Oaks, CA 91320-1799,
                                                                                                                                                                                                                                                                                                  58.4; DB 6
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                                         687
169
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 561
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                                                                                                                                                                                                                                                                     BP761124 mouse (C57BL/6) pancreatic islet library with recombination-based method Mus musculus cDNA clone mic01051 5',
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 302)
Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshio)
Takeda, J., Ohara, O. and Seino, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                       Mus musculus
                                                                                                                                                                                                                          BP761124
                                                                                                                                                                                                BP761124.1 GI:50219822
                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGAGCCCCGGCCCCAGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCCTGCCTGCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGAGGTGCTCCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCCGTGGAGACCCCGCTCCCCCCGGGGCTTAGGTCGGCGGGAGAGGAGGTAAGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGGGSGSGGGSGCGSGCCSGSGCGCGSCCCGCGGGGGGSGCSSGGGGCSGCCGS
                                                                                                                                                musculus (house mouse)
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ilarity 31.0%;
Conservative 8
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/db_xref="taxon:7227"
/clone=BaCR14B09"
/clone lib="RPCI-98"
/note="end: T7"
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Pred. No. 0.02:
81; Mismatches
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray Unpublished (2004)
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF535771 357 bp mRNA linear UI-M-GH0-cha-c-05-0-UI.rl NIH_BMAP_GH0 Mus musculus IMAGE:30533716 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                       sequence: 302-357, >(GGA)n#Simple_repeat
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 357)
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Fax: 81-78-382-5370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                         The following repetitive elements were found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGCTCCGGAGATCCCCAGTGGGACCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev stage="adult"
/dev stage="adult"
/clone lib="mouse (C57BL/6) pancreatic islet library with
/combination-based method"
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="mic01051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
     organism="Mus musculus"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="pancratic islet"
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CDNA clone
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                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF535776 361 bp
UI-M-GHO-Cha-C-15-0-UI.r1 NIH BMAP
IMAGE:30533726 5', mRNA sequence.
                                                The following repetitive elements were found in this cDNA sequence: 302-359, >(GGA)n#Simple_repeat Seq primer: pYX-5.
                                                                                                                                                                 Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 361)
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Mus musculus (house mouse)
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CF535776.1 GI:34587744
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/dev_gtage="1, 5, and 15 days newborn"
/lab_host="DH108 (T1 phage resistant)"
/clone_lib="NIH_BMAP_GH0"
/clone_lib="NIH_BMAP_GH0"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.34;
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REFERENCE AUTHORS TITLE

COMMENT

JOURNAL

FEATURES

RESULT 92 CF535776 LOCUS

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ACCESSION VERSION

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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 428)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

Waterston, R.

The WashU-HMI Mouse EST Project
                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA839768

428 bp mRNA linear EST 27-FEB-1998
vw51dll.rl Soares mammary_gland_NbMMG Mus musculus cDNA clone
tmAGE:12473 95' similar to TR:Q12873 Q12873 MI-2 AUTOANTIGEN 240
                                                                                                                                                                                                                                                                            Unpublished (1996)
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/dev stage="1, 5, and 15 days newborn"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP GH0"
/clone lib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lows Brain Anatomy Project (BMAP); 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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/strain="C57BL/6"
/db_xref="taxon:10090"
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                                                                                                                                                             St. Louis,
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                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                         CB520637

UI-M-G10-cej-l-03-0-UI.rl NIH_BMAP_GIO Mus musculus
IMAGE 6840436 5', mRNA sequence.
CB520637
CB520637.1 GI:29353992
EST.
                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
Unpublished (1999)
(BMAP)
The following repetitive elements were found sequence: 385-450, >(GGA)n#Simple_repeat
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 452)
                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:661037
                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCCTTCCACCTGGCCTGCCTGTCCCCTCCGGGAGATCCCCAGTGGGACCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCCTACCACCTCGTCTGCCTTGACCCCGAGCTTGACCAGGCTCCTGAGGGCAAGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: -28m13 rev2 ET from Amersham h quality sequence stop: 419.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:1247349"
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Pred. No. 0.02:
0; Mismatches
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                                                                                                                                                                                                                                     Collection
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CDNA clone
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REFERENCE
AUTHORS
TITLE
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CF911441
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VERSION
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MEDLINE
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Best Local
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Laboratory of Genetics
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, U
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0615 row: D column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 575)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA librar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A0615D04-5 NIA Mouse Hematopoietic Stem cDNA Library (Long 1) Mus musculus cDNA IMAGE:30749031 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq
                                                                                                                                                                                                                 Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF911441
CF911441.1
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                                                                                                                                                                                                                                                                                         21429098
                                                                                                                                                                                                                                                                                                                        Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                submicrogram amounts of total RNAs by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCTCCAGCTGCCAGGCAACAGTCCAGGAGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:6840436"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="eMbryo 13.5,14.5,16.5,17.5dpc"
/clone_lib="NHH_BMAP_GIO"
/clone_lib="NHH_BMAP_GIO"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pyx- Asc; Site_1: BcoR I;
/
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/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Cell (Lin-/c-Kit-/Sca-1+)
clone NIA:A0615D04
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RESULT 96
BU703948
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                                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                      ACCESSION
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   AUTHORS
TITLE
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Best Local
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                                                                                                                                                                              ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; (bases 1 to 690)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                           BU703948 690 bp mRNA linear EST 15-JUL-2003 UI-M-F00-bzr-e-16-0-UI.rl NIH_BMAP_F00 Mus musculus cDNA clone IMAGE 6406263 5', mRNA sequence.
BU703948
BU703948.1 GI:23631529
EST.
                                                                                                                                                                           Mus musculus
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High quality sequence stop: 575
                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCCTACCACCTCGTCTGCCTTGACCCCGAGCTTGACCGGGCTCCTGAGGGCAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inter-Vector: pCWV-SPORTS (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [pMID: 11544199]). Total
RNAs were obtained from Drs. Dennis Taub, Dan Longo
(National Institute on Aging, USA), Jonathan Keller
(National Cancer Institute, USA), Jonathan Keller
(DAS were amplified by purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pcMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.2 kb. The library was
constructed by Yulan Plao."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Age ~10 weeks old"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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58.3%;
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                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 GGTGCTCCAGCTGCCTGCAGGCAACAGTCCAGGAGGTGCAGCCCCGGGCAGAGGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 AGGACGAGTGTGCCGTGTGTCGGGACGGCGGGGAGCTCATCTGCTGTGACGGCTGCCCTC
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AK0454
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Mus musculus (house mouse)
                                                                               HTC; CAP trapper.
                                                                                                                                                                                 AK045449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       >(GGA)n#Simple_repeat
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                              AK045449.1 GI:26337378
                                                                                                                                                                                                                      insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the Tu a Clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The following repetitive elements were found in this cDNA equence: 1-42, >(CAG)n#Simple_repeat 647-690,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGATTACTGTGAGGTGTGCCAGCAGGGCGGGGAAATTATTCTGTGCGACACCCTGCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="whole brain"
/dev_stage="embryo 12.5dpc"
/lab_host="PH10B (TI phage resistant)"
/clone lib="NIH BMAP FOO"
/clone lib="NIH BMAP FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
Site_2: Not I; The library was constructed according
Sonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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/strain="C57BL/6"
/db_xref="taxon:10090"
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Pred. No. 0.022;
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[Homo sapiens], full
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                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2253)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FANTOM Consortium. Functional annotation of a full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                     URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                     prepare mouse tissues.
Please visit our web site for further details
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                                                                                                                                                                                                                                                    Division of Experimental Animal Research
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organism="Mus musculus"
/mol_type="mRNA"
                                                                                            Location/Qualifiers
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          BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo:
Eukaryota, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                    CNS0072Q 932 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                       AL066742.1
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evidence: FASTY, 96
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protein (fragment) homolog [Homo sapiens] (PIR|I38558,
evidence: FASTY, 96.8%ID, 98.4%length, match=1578)
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/db_xref="FANTOM_DB:B230201M16"
/db_xref="taxon:10090"
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clone_lib="RIKEN full-length enric"
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http://www.fruitfly.org The
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                                                                                               Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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AG057392
AG057392.1 GI:16594851
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Totoki, Y., Watanabe, H. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/mol_type="genomic_DNA"
/db_xref="taxon:7227"
/clone="BACR14B09"
/clone=lib="RPCI-98"
/note="end : T7"
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AGENCOURT_8803230 Lupski_sciatic_nerve Homo
IMAGE:6198951 5', mRNA sequence.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC was generated during the R&D process and may have higher chance clone tracking errors.
                                                       BQ953925.1
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                             Homo sapiens (human)
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R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DN/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="PTB-043P11.R"
                                                       GI:22369403
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AGGAGGTAAGAGGTCCACCTAGGGGAACCCCTAGCC AGCACCTTGCCGCGCTCCGCCCTTCTTGCAGCCC AGCACCTTGCCGCGCTCCGCCCTCCCGCCCCCAGCGTT CCTGCACCCCCTACTGTGTGTGGGTCCTGAGGGTT CCTGCACCCCCTACCTGTGTGTGGGTCCTGAGGGTT CTGCACCCCCCCGCCGCCGCCGCGGCCGGCCGGGCTGCTGCTGCT	944 855 804 915 915	615 769 675 829 735	
CGCCGGGGNCACGACTCTTGTCTACA 828	TTGCGGGGTTGCGGAGATGGTACGGACGTGCTGCGGTGTACTCACTGCGCCGCTGCCTT	CGCGGCGGGGGGCCCCCCCGCCCCCCCCCGCCGCCGCNCNGGGGCCCCCGCGNCGGGCCCGCGCCCCCGCCG	

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Search completed: February 9, 2005, 17:40:05 Job time : 4565 secs